

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____

Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 02-10-03
Searcher: Beverly C 4499
Terminal time: 25
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Search Site

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Type of Search

_____ N.A. Sequence
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_____ Structure
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Vendors

_____ IG Suite
_____ STN
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_____ Geninfo
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_____ DARC/Questel
_____ Other: CGN

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2003, 08:35:55 ; Search time 2704 Seconds

(without alignments)
9288.358 Million cell updates/sec

Title: US-10-021-811-35

Sequence: 1 gccagagctctatcacacac.....aaaaaaaaaaaaaaaa 863

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:.*
1: gb_da.*
2: gb_hcg.*
3: gb_in.*
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6: gb_pat.*
7: gb_ph.*
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9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_da.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
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27: em_sts.*
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32: em_hcg_other.*
33: em_hcg_mus.*
34: em_hcg_pln.*
35: em_hcg_rnd.*
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37: em_hcg_vrt.*
38: em_sy.*
39: em_hcg_hum.*
40: em_hcg_mus.*
41: em_hcg_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	4.9	52514	2 AC116551	AC116551 Dictyoste
2	41	4.8	1455	BC009883	BC009883 Homo sapi
3	41	4.8	2037	6 AX317981	AX317981 Sequence
4	41	4.8	2097	3 AB079606	AB079606 Dictyoste
5	41	4.8	2307	6 AB1160	AB1160 Sequence 5
6	41	4.8	4329	6 AB1162	AB1162 Sequence 7
7	40	4.6	1856	3 AY051514	AY051514 Drosophi
8	40	4.6	2472	9 BC025672	BC025672 Homo sapi
9	40	4.6	10825	6 AX344799	AX344799 Sequence
10	39	4.5	200	11 G38015	G38015 C1M31 plasm
11	39	4.5	236	11 G37836	G37836 wh_hspi pla
12	39	4.5	415	8 AB072484	AB072484 Lycopersi
13	39	4.5	691	3 AY070797	AY070797 Drosophi
14	39	4.5	988	10 BC028785	BC028785 Mus muscu
15	39	4.5	1121	9 AF236637	AF236637 Homo sapi
16	39	4.5	1373	8 AY124468	AY124468 Heyera bra
17	39	4.5	1470	9 BC012575	BC012575 Homo sapi
18	39	4.5	2547	3 PFGRPXA	PFGRPXA
19	39	4.5	2554	3 AF106064	AF106064 Plasmodu
20	39	4.5	3001	6 AX344925	AX344925 Sequence
21	39	4.5	5273	6 AX345777	AX345777 Sequence
22	39	4.5	5313	6 AX345665	AX345665 Sequence
23	39	4.5	6120	6 AX323825	AX323825 Sequence
24	39	4.5	6120	6 AX344894	AX344894 Sequence
25	39	4.5	6476	6 HSM803020	AL171373 Homo sapi
26	39	4.5	6956	6 AX348657	AX348657 Sequence
27	39	4.5	7046	6 AX344880	AX344880 Sequence
28	39	4.5	7890	6 AX251883	AX347018 Sequence
29	39	4.5	7890	6 AX251883	AX251883 Sequence
30	39	4.5	8246	6 AX345105	AX348672 Sequence
31	39	4.5	8246	6 AX345107	AX345105 Sequence
32	39	4.5	8372	6 AX251107	AX251107 Sequence
33	39	4.5	9963	6 AX345596	AX345596 Sequence
34	39	4.5	11178	6 AX344168	AX251754 Sequence
35	39	4.5	11178	6 AX344168	AX344168 Sequence
36	39	4.5	11178	6 AX348939	AX348939 Sequence
37	39	4.5	13427	6 AX346828	AX346828 Sequence
38	39	4.5	14923	3 AE001394	AE001394 Plasmodu
39	39	4.5	14955	3 AF000580	AF000580 Dictyoste
40	39	4.5	14955	3 AF000580	AF000580 Dictyoste
41	39	4.5	15500	6 AX251262	AX251262 Sequence
42	39	4.5	17234	6 AX458502	AX458502 Sequence
43	39	4.5	17389	6 AX346316	AX346316 Sequence
44	39	4.5	35119	2 AC116958	AC116958 Dictyoste
45	39	4.5	80472	8 F24J2	AF262039 Arabidops
46	39	4.5	96136	2 AC097674	AC097674 Rattus no
47	39	4.5	97683	2 AC116548	AC116548 Dictyoste
48	39	4.5	98734	2 PFMALIP2	AL031745 Plasmodu
49	39	4.5	101567	2 AL645510	AL645510 Dario rer
50	39	4.5	113880	3 PFMALJP4	AL008970 Plasmodu
51	39	4.5	116696	3 PFMALJP3	Z98547 Plasmodu
52	39	4.5	137526	2 AC025902	AC125902 Rattus no
53	39	4.5	205429	2 AC005506	AC005506 Plasmodu
54	39	4.5	205429	2 AC005506	AC005506 Plasmodu
55	39	4.5	216100	2 AC129180	AC129180 Mus muscu
56	39	4.5	232519	2 AC095709	AC095709 Rattus no
57	39	4.5	234112	3 PFMALJP2	AL035475 Plasmodu
58	39	4.5	349980	6 AX344566	AX344566 Sequence
59	39	4.5	349980	6 AX344567	AX344567 Sequence
60	38	4.4	501	8 AF048745	AF048745 Phycolac
61	38	4.4	609	3 TRBSLXA	X00632 T. cruzi sma
62	38	4.4	1588	3 AY069348	AY069348 Drosophi
63	38	4.4	2120	9 BC008496	BC008496 Homo sapi
64	38	4.4	2120	9 BC008496	BC008496 Homo sapi
65	38	4.4	2682	9 BC014993	BC014993 Homo sapi

66	38	4.4	4197	3	AF163835	AF163835 Dictyoste	C	139	36	4.2	314	11	G25310	G25310 human SRS E
67	38	4.4	4446	3	DDU72236	DDU72236 Dictyosteli	C	140	36	4.2	332	6	AX187103	AX187103 Sequence
68	38	4.4	5447	6	AX251515	AX251515 Sequence	C	141	36	4.2	414	3	AF159579	AF159579 Butrus ma
69	38	4.4	6386	9	HSMB80518	AX1832211 Homo sapi	C	142	36	4.2	414	3	AF159579	G33458 human SRS S
70	38	4.4	7133	12	CUPYBULCBX	125833 Cloning vec	C	143	36	4.2	500	11	G33458	G29359 human SRS S
71	38	4.4	7805	8	YSCDUD21NU	LI9873 Yeast pYEU	C	144	36	4.2	513	11	G29359	AXJ32735 Homo sapi
72	38	4.4	9770	6	AX344934	AX344934 Sequence	C	145	36	4.2	778	9	AK026857	AK026857 Homo sapi
73	38	4.4	17480	3	AC114258	AC114258 Dictyoste	C	146	36	4.2	838	9	AY061350	AY061350 Drosophila
74	38	4.4	19798	6	AX164588	AX164588 Sequence	C	147	36	4.2	840	8	CNS0180K	AY110675 Botrytis
75	38	4.4	19912	6	AX164586	AX164586 Sequence	C	148	36	4.2	963	3	AY1186596	AY118659 Drosophila
76	38	4.4	20160	6	AX164590	AX164590 Sequence	C	149	36	4.2	1007	6	AR205208	AR205208 Sequence
77	38	4.4	20217	6	AX164594	AX164594 Sequence	C	150	36	4.2	1007	6	AR205208	AR205208 Sequence
78	38	4.4	20247	6	AX164592	AX164592 Sequence	C	151	36	4.2	1033	3	AY128476	AY128476 Drosophila
79	38	4.4	20316	6	AX164592	AX164592 Sequence	C	152	36	4.2	1062	9	BC004155	BC004155 Homo sapi
80	38	4.4	104992	2	AC005504	AC005504 Plasmodin	C	153	36	4.2	1072	10	BC0083919	BC0083919 Mus muscu
81	38	4.4	141226	2	AC004710	AC004710 Plasmodin	C	154	36	4.2	1097	10	BC0083919	BC0083919 Mus muscu
82	38	4.4	123160	2	AL353719	AL353719 Human DNA	C	155	36	4.2	1120	9	HSMB801270	HSMB801270
83	38	4.4	169546	2	AC004157	AC004157 Plasmodin	C	156	36	4.2	1127	9	BC031545	BC031545
84	38	4.4	171187	2	AC116960	AC116960 Dictyoste	C	157	36	4.2	1138	9	HSMB802391	HSMB802391
85	38	4.4	178273	2	AC005508	AC005508 Plasmodin	C	158	36	4.2	1153	9	AK027115	AK027115 Homo sapi
86	38	4.4	196490	2	AC005507	AC005507 Plasmodin	C	159	36	4.2	1176	9	IR07483647	IR07483647
87	37	4.3	441	11	G73684	G73684 RZ976R etio	C	160	36	4.2	1193	9	HSMB801955	HSMB801955
88	37	4.3	819	3	AF246695	AF246695 Bombyx mo	C	161	36	4.2	1214	3	AY075185	AY075185
89	37	4.3	900	9	BC030229	BC030229 Homo sapi	C	162	36	4.2	1222	3	AY075185	AY075185
90	37	4.3	1137	9	HSU66818	U66818 Human ubiq	C	163	36	4.2	1232	3	HSMB801798	HSMB801798
91	37	4.3	1168	9	BC005085	BC005085 Homo sapi	C	164	36	4.2	1232	3	AF448505	AF448505 Homo sapi
92	37	4.3	1206	8	ATRNEX	X99224 A. thaliana	C	165	36	4.2	1268	8	AF448505	AF448505 Brassaica
93	37	4.3	1260	9	BC007235	BC007235 Homo sapi	C	166	36	4.2	1270	8	AF448505	AF448505 Drosophila
94	37	4.3	1261	3	DDIADCVAO1	LO5496 Dictyosteli	C	167	36	4.2	1279	6	AX086727	AX086727 Sequence
95	37	4.3	1492	8	HAV91341	U19341 Helianthus	C	168	36	4.2	1321	9	AY119217	AY119217 Sequence
96	37	4.3	1525	8	AF251264	AF251264 Trilicium	C	169	36	4.2	1384	8	AF193053	AF193053 Homo sapi
97	37	4.3	1700	8	AF321556	AF321556 Trilicium	C	170	36	4.2	1419	8	CCCHSMR	CCCHSMR
98	37	4.3	1718	9	AK025339	AK025339 Homo sapi	C	171	36	4.2	1428	3	DMRSSMR	DMRSSMR
99	37	4.3	1759	6	AX100593	AX100593 Sequence	C	172	36	4.2	1432	3	AF273828	AF273828 Mus muscu
100	37	4.3	1856	9	AF394451	AF394451 Mus muscu	C	173	36	4.2	1454	10	BC028987	BC028987 Mus muscu
101	37	4.3	1856	9	HSU66867	U66867 Human ubiq	C	174	36	4.2	1501	3	BC015453	BC015453 Homo sapi
102	37	4.3	1867	10	BC005637	BC005637 Mus muscu	C	175	36	4.2	1542	3	AY070834	AY070834 Drosophila
103	37	4.3	1969	5	AY036624	AY036624 Dario rer	C	176	36	4.2	1551	10	MMU291757	MMU291757
104	37	4.3	2008	3	AF145689	AF145689 Drosophila	C	177	36	4.2	1600	6	BC032456	BC032456
105	37	4.3	2290	3	AY119138	AY119138 Drosophila	C	178	36	4.2	1614	9	BC032456	BC032456
106	37	4.3	2441	3	DDU67940	U67940 Dictyosteli	C	179	36	4.2	1616	10	BC021155	BC021155 Mus muscu
107	37	4.3	2832	4	AP288406	AF288406 Homo sapi	C	180	36	4.2	1631	6	AX036060	AX036060 Sequence
108	37	4.3	3366	5	AF051786	AF051786 Xenopus 1	C	181	36	4.2	1654	3	AF503909	AF503909 Homo sapi
109	37	4.3	9750	12	AF025397	U86815 Expression	C	182	36	4.2	1736	6	AR119632	AR119632 Sequence
110	37	4.3	9763	12	EVU68615	U86815 Expression	C	183	36	4.2	1736	6	AR119632	AR119632 Sequence
111	37	4.3	9763	12	AF126280	AF126280 Expression	C	184	36	4.2	1736	6	AR119632	AR119632 Sequence
112	37	4.3	10136	6	135495	135495 Sequence 2	C	185	36	4.2	1736	6	AR169113	AR169113 Sequence
113	37	4.3	10765	12	EVU67875	U67875 pBSP-1 year	C	186	36	4.2	1736	6	AR169113	AR169113 Sequence
114	37	4.3	12029	3	AB001381	AB001381 Plasmodin	C	187	36	4.2	1865	10	BC016526	BC016526 Mus muscu
115	37	4.3	27785	2	AC116978	AC116978 Dictyoste	C	188	36	4.2	1940	10	BC026886	BC026886
116	37	4.3	45296	2	AC116978	AC116978 Dictyoste	C	189	36	4.2	1958	3	AF242200	AF242200 Bombyx mo
117	37	4.3	56152	2	AC116963	AC116963 Dictyoste	C	190	36	4.2	1962	3	AY060994	AY060994 Drosophila
118	37	4.3	56152	6	AX251552	AX251552 Sequence	C	191	36	4.2	1973	9	AB063088	AB063088 Macaca fa
119	37	4.3	84759	2	AP000730	AP000730 Homo sapi	C	192	36	4.2	2096	9	BC022483	BC022483 Homo sapi
120	37	4.3	84805	2	AC116918	AC116918 Dictyoste	C	193	36	4.2	2130	9	BC025751	BC025751 Homo sapi
121	37	4.3	106144	2	AC116425	AC116425 Dictyoste	C	194	36	4.2	2248	9	AK025239	AK025239 Homo sapi
122	37	4.3	110000	2	AC0984053_1	Continuation (2 of	C	195	36	4.2	2253	9	BC032682	BC032682 Homo sapi
123	37	4.3	110000	2	AC0984053_1	Continuation (2 of	C	196	36	4.2	2301	5	AF045607	AF045607 Xenopus 1
124	37	4.3	120240	2	AP000627	AP000627 Homo sapi	C	197	36	4.2	2318	3	DDU6425	DDU6425 Drosophila
125	37	4.3	133501	2	AC116956	AC116956 Dictyoste	C	198	36	4.2	2349	3	AY060425	AY060425
126	37	4.3	164599	2	AC068971	AC068971 Homo sapi	C	199	36	4.2	2394	9	HSMB805513	HSMB805513
127	37	4.3	166125	2	AC019327	AC019327 Homo sapi	C	200	36	4.2	2427	9	AK020310	AK020310 Homo sapi
128	37	4.3	167357	2	AC0955771	AC0955771 Homo sapi	C	201	36	4.2	2430	9	AK074464	AK074464 Homo sapi
129	37	4.3	169547	2	AC095580	AC095580 Rattus no	C	202	36	4.2	2450	5	AF287007	AF287007 Dario rer
130	37	4.3	170001	2	AC116086	AC116086 Rattus no	C	203	36	4.2	2510	9	BC014039	BC014039 Homo sapi
131	37	4.3	179786	2	AP001015	AP001015 Homo sapi	C	204	36	4.2	2531	4	BC027040	BC027040 Homo sapi
132	37	4.3	196827	2	AC107825	AL391335 Mus muscu	C	205	36	4.2	2714	4	BTU75304	BTU75304 Bos taurus
133	37	4.3	202290	2	AL391335	AL391335 Homo sapi	C	206	36	4.2	2720	9	BC007575	BC007575 Homo sapi
134	37	4.3	217726	2	AC127573	AC127573 Mus muscu	C	207	36	4.2	2927	3	AY118573	AY118573
135	37	4.3	253751	2	AC051621	AC051621 Mus muscu	C	208	36	4.2	3065	14	LRYBABC	LRYBABC
136	37	4.3	259854	2	AC098462	AC098462 Rattus no	C	209	36	4.2	3196	9	AF355402	AF355402 Homo sapi
137	36	4.2	80	6	A08907	A08907 H. sepiens (C	210	36	4.2	3295	9	AF070673	AF070673 Homo sapi
138	36	4.2	140	3	DMRRNL	X08015 Drosophila	C	211	36	4.2	3508	3	AF023665	AF023665 Plasmodin

212	36	4.2	3523	9	BC027936	285	35	4.1	570	6	118355	118355	Sequence	10
213	36	4.2	3618	9	BC028036	286	35	4.1	570	6	121342	121342	Sequence	10
214	36	4.2	3649	8	AB049934	287	35	4.1	570	6	140331	140331	Sequence	10
215	36	4.2	4108	10	BC008515	288	35	4.1	570	6	AF137353	AF137353	Piem sat	
216	36	4.2	4421	9	HSB002480	289	35	4.1	609	8	AR085690	AR085690	Sequence	
217	36	4.2	5008	9	HSB005526	290	35	4.1	609	6	114392	114392	Sequence	9
218	36	4.2	5750	6	AX251465	291	35	4.1	629	9	AK026557	AK026557	Strongylo	
219	36	4.2	5750	6	AX346910	292	35	4.1	639	3	AF035657	AF035657	Strongylo	
220	36	4.2	5829	6	AX346628	293	35	4.1	645	8	AY070103	AY070103	Arbidiops	
221	36	4.2	6887	6	AX344607	294	35	4.1	658	8	BC009561	BC009561	Homo sapi	
222	36	4.2	8392	6	AX346392	295	35	4.1	760	6	AR051976	AR051976	Sequence	
223	36	4.2	8606	3	TPY238858	296	35	4.1	760	6	1152150	1152150	Sequence	49
224	36	4.2	9731	6	AX345892	297	35	4.1	767	3	AT118824	AT118824	Drosophill	
225	36	4.2	12029	3	AE001405	298	35	4.1	791	8	OSA004966	OSA004966	Oryza sat	
226	36	4.2	12706	3	AC115581	299	35	4.1	792	9	AK026506	AK026506	Homo sapi	
227	36	4.2	32070	2	AC116983	300	35	4.1	822	8	AF395880	AF395880	Oryza sat	
228	36	4.2	39369	2	AC115681	301	35	4.1	843	3	AY118774	AY118774	Drosophill	
229	36	4.2	43993	2	AC116965	302	35	4.1	844	9	BC018536	BC018536	Homo sapi	
230	36	4.2	52514	2	AC116551	303	35	4.1	887	9	BC012470	BC012470	Homo sapi	
231	36	4.2	53440	2	AC117078	304	35	4.1	944	3	AY118333	AY118333	Drosophill	
232	36	4.2	56099	2	AC115598	305	35	4.1	945	3	AF457546	AF457546	Anopheles	
233	36	4.2	105470	2	AC116306	306	35	4.1	964	3	BC005114	BC005114	Homo sapi	
234	36	4.2	106434	3	AC117080	307	35	4.1	973	10	AF020524	AF020524	Mus muscu	
235	36	4.2	110000	2	AC109772_0	308	35	4.1	978	9	HSB000758	HSB000758	Homo sapi	
236	36	4.2	110000	2	PFMAL4P1_1	309	35	4.1	980	5	AF157110	AF157110	Danio rer	
237	36	4.2	113880	2	PFMAL3P4	310	35	4.1	986	3	AY113296	AY113296	Drosophill	
238	36	4.2	124820	2	AC117073	311	35	4.1	1116	8	OSA237661	OSA237661	Oryza sat	
239	36	4.2	129360	2	AC117079	312	35	4.1	1160	6	AR112636	AR112636	Sequence	
240	36	4.2	131397	2	CNS08C9D	313	35	4.1	1186	9	HSN420453	HSN420453	Homo sapi	
241	36	4.2	131397	2	CNS08C9D	314	35	4.1	1196	8	AY130289	AY130289	Homo sapi	
242	36	4.2	132000	2	AC116976	315	35	4.1	1234	3	AY119240	AY119240	Arbidiops	
243	36	4.2	135581	2	AP000771	316	35	4.1	1240	3	TBU72205	TBU72205	Typanosoma	
244	36	4.2	136755	2	CNS08C86	317	35	4.1	1281	10	BC029254	BC029254	Mus muscu	
245	36	4.2	144826	2	CNS08C86	318	35	4.1	1312	6	AX306543	AX306543	Sequence	
246	36	4.2	148312	2	AC101906	319	35	4.1	1316	9	AK027106	AK027106	Homo sapi	
247	36	4.2	149583	2	AC128560	320	35	4.1	1327	6	AX094799	AX094799	Sequence	
248	36	4.2	160759	2	AC117082	321	35	4.1	1334	9	BC008673	BC008673	Homo sapi	
249	36	4.2	164520	2	AC020738	322	35	4.1	1337	9	AF098798	AF098798	Homo sapi	
250	36	4.2	165353	9	AC023822	323	35	4.1	1341	9	AF029689	AF029689	Homo sapi	
251	36	4.2	167303	9	AP001877	324	35	4.1	1358	6	AX347225	AX347225	Sequence	
252	36	4.2	170168	2	AC115313	325	35	4.1	1388	9	AK027096	AK027096	Homo sapi	
253	36	4.2	174900	2	AC110319	326	35	4.1	1391	9	BC032596	BC032596	Homo sapi	
254	36	4.2	178273	2	AC005308	327	35	4.1	1425	8	SOTSXK3	SOTSXK3	Glycine max	
255	36	4.2	179335	9	AP000870	328	35	4.1	1432	3	AY069596	AY069596	Drosophill	
256	36	4.2	181200	3	AC099365	329	35	4.1	1481	3	AY061988	AY061988	Epiphyas	
257	36	4.2	181636	3	AC0088224	330	35	4.1	1482	9	BC004991	BC004991	Homo sapi	
258	36	4.2	183457	2	AC111038	331	35	4.1	1495	5	AP306736	AP306736	Xenopus l	
259	36	4.2	184703	2	ALU773566	332	35	4.1	1544	3	AY075259	AY075259	Drosophill	
260	36	4.2	189303	2	AC107114	333	35	4.1	1550	9	HSKMR9	HSKMR9	H. sapiens m	
261	36	4.2	193308	2	AC073679	334	35	4.1	1584	10	HAU8B1M	HAU8B1M	H. annuus Ub	
262	36	4.2	200776	2	AC107841	335	35	4.1	1584	10	AF083032	AF083032	Mus muscu	
263	36	4.2	202785	2	AC109204	336	35	4.1	1590	8	BC003614	BC003614	Homo sapi	
264	36	4.2	203437	2	AC125468	337	35	4.1	1613	9	AF014801	AF014801	Eschschol	
265	36	4.2	212368	2	AC102048	338	35	4.1	1619	9	BC032001	BC032001	Homo sapi	
266	36	4.2	212139	2	AC022129	339	35	4.1	1627	9	BC023977	BC023977	Homo sapi	
267	36	4.2	222045	2	AC023354	340	35	4.1	1629	9	BC026015	BC026015	Homo sapi	
268	36	4.2	225448	2	PFMAL4P4	341	35	4.1	1636	3	CEU60058	CEU60058	Caenorhabdi	
269	36	4.2	226509	2	AC079490	342	35	4.1	1667	9	HSU90912	HSU90912	Human clone	
270	36	4.2	229487	2	AC095711	343	35	4.1	1682	9	BC016047	BC016047	Homo sapi	
271	36	4.2	234267	2	AC127293	344	35	4.1	1698	8	AF230740	AF230740	Euphorbia	
272	36	4.2	234267	2	AC127293	345	35	4.1	1703	9	BC002370	BC002370	Homo sapi	
273	36	4.2	236365	2	AC087099	346	35	4.1	1722	9	AB048919	AB048919	Macaaca fa	
274	36	4.2	268147	2	AC116966	347	35	4.1	1739	9	BC031645	BC031645	Homo sapi	
275	36	4.2	268147	2	AC116966	348	35	4.1	1740	6	A37880	A37880	Sequence	2
276	35	4.1	278	6	AX185578	349	35	4.1	1740	6	A95149	A95149	Sequence	2
277	35	4.1	285	6	BC011247	350	35	4.1	1740	6	AR157917	AR157917	Sequence	3
278	35	4.1	314	6	AX331680	351	35	4.1	1740	6	ATAP2	ATAP2	Sequence	3
279	35	4.1	314	11	G21431	352	35	4.1	1740	8	X71787	X71787	A. thaliana	
280	35	4.1	444	8	AF105432	353	35	4.1	1743	3	AY070515	AY070515	Drosophill	
281	35	4.1	500	8	AF242374	354	35	4.1	1749	8	AF249299	AF249299	Cunningha	
282	35	4.1	546	10	BC026533	355	35	4.1	1765	10	BC034838	BC034838	Mus muscu	
283	35	4.1	548	9	BC001700	356	35	4.1	1784	10	BC030456	BC030456	Mus muscu	
284	35	4.1	556	9	AB055361	357	35	4.1	1813	9	BC011187	BC011187	Homo sapi	

358	35	4.1	1833	9	BC008640	Homo sapi	431	2930	9	AF195092	AF195092 Homo sapi
359	35	4.1	1845	3	AY069470	Drosophila	432	2975	9	HSMB04650	AF133337 Homo sapi
360	35	4.1	1864	3	AB056421	Macaca fa	433	2992	3	AF012945	AF012945 Dictyoste
361	35	4.1	1884	3	AB088425	Bombyx mo	434	3037	3	HSMB03746	AF132438 Homo sapi
362	35	4.1	1892	3	AK025387	Homo sapi	435	3107	6	AB4105	AB4105 Sequence 9
363	35	4.1	1892	10	BC018278	Mus muscu	436	3152	8	BC014305	BC014305 Homo sapi
364	35	4.1	1899	9	BC033675	Homo sapi	437	3214	8	AF203700	AF203700 Phaeo
365	35	4.1	1907	9	BC033684	Homo sapi	438	3245	9	BC013579	BC013579 Homo sapi
366	35	4.1	1915	6	AF110640	Homo sapi	439	3353	9	HSMB03622	HSMB03622 Homo sapi
367	35	4.1	1931	6	AF183234	Homo sapi	440	3379	9	HSMB04444	AF133333 Homo sapi
368	35	4.1	1931	6	AB020634	Sequence	441	3405	3	AY119601	AY119601 Drosophila
369	35	4.1	1931	6	AB082199	Sequence	442	3669	9	HSMB05593	BC009989 Homo sapi
370	35	4.1	1950	3	AF182283	Boophilus	443	3781	9	BC009989	BC009989 Homo sapi
371	35	4.1	1951	10	BC016285	Homo sapi	444	3905	6	A03736	A03736 H sapiens m
372	35	4.1	1960	10	BC021360	Mus muscu	445	3905	6	A11790	A11790 H sapiens m
373	35	4.1	1975	3	AB072307	Bombyx mo	446	3930	10	BC029763	BC029763 Mus muscu
374	35	4.1	1980	3	BC033790	Homo sapi	447	3980	5	EC027963	EC027963 Homo sapi
375	35	4.1	1999	10	MMU80780	Homo sapi	448	3980	5	AF064799	AF064799 Danio rer
376	35	4.1	2005	9	BC027939	Sequence	449	4018	3	AF362370	AF362370 Dictyoste
377	35	4.1	2007	6	AF170139	Sequence	450	4028	3	AF003106	AF003106 Drosophila
378	35	4.1	2007	6	AF170140	Sequence	451	4045	6	AX356495	AX356495 Sequence
379	35	4.1	2029	3	AB069422	Drosophila	452	4120	8	OSG062	Y12595 O. sativa nr
380	35	4.1	2048	9	BC013002	Homo sapi	453	4193	9	AF017789	AF017789 Homo sapi
381	35	4.1	2059	10	BC014802	Mus muscu	454	4407	6	AX086676	AX086676 Sequence
382	35	4.1	2066	9	BC002611	Homo sapi	455	4434	9	HSMB01973	HSMB01973 Homo sapi
383	35	4.1	2126	10	BC024858	Mus muscu	456	4452	10	AF054831	AF054831 Mus muscu
384	35	4.1	2132	10	BC026639	Mus muscu	457	4574	9	HSMB03437	HSMB03437 Homo sapi
385	35	4.1	2150	9	AB070072	Macaca fa	458	4629	9	HSMB04034	HSMB04034 Homo sapi
386	35	4.1	2163	3	AF255674	Drosophila	459	4702	10	BC030304	BC030304 Mus muscu
387	35	4.1	2207	3	AB065434	Homo sapi	460	4759	3	DMUS3AP6	Y12322 D. melanogast
388	35	4.1	2228	10	BC015289	Mus muscu	461	5001	3	PFABRA	M2425 Homo sapien
389	35	4.1	2254	9	BC006652	Mus muscu	462	5312	3	AF241823	AF241823 Dictyoste
390	35	4.1	2264	9	BC003065	Homo sapi	463	5390	3	AY119181	AY119181 Drosophila
391	35	4.1	2279	10	BC025490	Mus muscu	464	5890	3	DDU60086	DDU60086 Dictyoste
392	35	4.1	2366	9	BC034043	Homo sapi	465	6045	6	AX344536	AX344536 Sequence
393	35	4.1	2400	6	AS5845	Sequence 1	466	6045	6	AX349055	AX349055 Sequence
394	35	4.1	2400	8	NPZEXANT	X95732 N. plumbagin	467	6204	6	HSMB03878	HSMB03878 Homo sapi
395	35	4.1	2403	9	AF255309	AF255309 Homo sapi	468	7622	3	AF112367	AF112367 Sequence
396	35	4.1	2413	3	HSMB01715	AF113674 Homo sapi	469	8093	6	AX251189	AX251189 Sequence
397	35	4.1	2413	3	AY118685	Drosophila	470	8093	6	AX281166	AX281166 Sequence
398	35	4.1	2452	3	AF337815	AF337815 Dictyoste	471	8093	6	AX347410	AX347410 Sequence
399	35	4.1	2462	9	BC016388	BC016388 Homo sapi	472	8548	3	AX356411	AX356411 Sequence
400	35	4.1	2485	9	AK094962	Homo sapi	473	8649	6	AX251388	AX251388 Sequence
401	35	4.1	2517	9	BC011872	Homo sapi	474	8649	6	AX251856	AX251856 Sequence
402	35	4.1	2518	10	BC018260	Mus muscu	475	8649	6	AX344242	AX344242 Sequence
403	35	4.1	2530	9	AK000309	AK000309 Homo sapi	476	8649	6	AX346333	AX346333 Sequence
404	35	4.1	2536	9	BC007315	BC007315 Homo sapi	477	8649	6	AX251977	AX251977 Sequence
405	35	4.1	2541	9	AB050450	AB050450 Homo sapi	478	8649	6	AX346339	AX346339 Sequence
406	35	4.1	2546	9	AB055293	AB055293 Macaca fa	479	8649	6	AX346337	AX346337 Sequence
407	35	4.1	2558	9	BC030525	BC030525 Homo sapi	480	8649	6	AX251083	AX251083 Sequence
408	35	4.1	2592	9	BC012807	BC012807 Homo sapi	481	8649	6	AX251856	AX251856 Sequence
409	35	4.1	2600	3	AY060298	AY060298 Homo sapi	482	8649	6	AX346337	AX346337 Sequence
410	35	4.1	2640	9	AF184965	AF184965 Homo sapi	483	8649	6	AX346339	AX346339 Sequence
411	35	4.1	2643	9	HSU09366	HSU09366 Homo sapi	484	8649	6	AX346333	AX346333 Sequence
412	35	4.1	2649	10	BC027311	BC027311 Mus muscu	485	8649	6	AX251977	AX251977 Sequence
413	35	4.1	2653	3	AY089530	AY089530 Drosophila	486	8649	6	AX346339	AX346339 Sequence
414	35	4.1	2663	3	AF337552	AF337552 Drosophila	487	8649	6	AX346337	AX346337 Sequence
415	35	4.1	2728	9	BC018396	BC018396 Homo sapi	488	8649	6	AX346339	AX346339 Sequence
416	35	4.1	2738	9	AB029891	AB029891 Homo sapi	489	8649	6	AX346337	AX346337 Sequence
417	35	4.1	2768	5	AB044143	AB044143 Cynops py	490	10091	3	AC115589	AC115589 Sequence
418	35	4.1	2782	9	HSMB03706	HSMB03706 Homo sapi	491	10957	6	AX251083	AX251083 Sequence
419	35	4.1	2807	9	AY038999	AY038999 Homo sapi	492	11523	6	AX278012	AX278012 Sequence
420	35	4.1	2814	6	AX335827	AX335827 Homo sapi	493	11523	6	AX323709	AX323709 Sequence
421	35	4.1	2814	6	AX410773	AX410773 Sequence	494	11523	6	AX346824	AX346824 Sequence
422	35	4.1	2814	6	AX454750	AX454750 Sequence	495	11523	6	AX347440	AX347440 Sequence
423	35	4.1	2814	6	AX491228	AX491228 Sequence	496	11523	6	AX349161	AX349161 Sequence
424	35	4.1	2814	6	HSU73682	HSU73682 Homo sapi	497	12029	3	AB001389	AB001389 Sequence
425	35	4.1	2832	8	BC003770	BC003770 Mus muscu	498	12226	14	RTUPOXP	M95197 Rice tungro
426	35	4.1	2851	10	OSG061	Y12594 O. sativa nr	499	12601	3	AX347108	AX347108 Sequence
427	35	4.1	2853	9	AF015041	AF015041 Homo sapi	500	13674	3	U00691	U00691 Dictyoste
428	35	4.1	2863	9	HSMB02338	HSMB02338 Homo sapi	501	13729	3	U00796	U00796 Dictyoste
429	35	4.1	2861	10	BC020176	BC020176 Mus muscu	502	13951	3	AB001406	AB001406 Plasmodiu
430	35	4.1	2918	3	AY061485	AY061485 Drosophila	503	14514	2	AC115610	AC115610 Dictyoste

504	35	4.1	14529	3	AE001397	AE001397 Plasmodiu	C 577	35	4.1	154583	10	AL672156	AL672156 Mouse DNA
505	35	4.1	14222	3	AE001421	AE001421 Plasmodiu	C 578	35	4.1	155359	9	AP003689	AP003689 Homo sapi
C 506	35	4.1	21537	6	AX346901	AX346901 Sequence	C 579	35	4.1	156060	2	AC004153	AC004153 Plasmodiu
C 507	35	4.1	27291	2	AC115575	AC115575 Dictyoste	C 580	35	4.1	156060	2	AC004153	AC004153 Plasmodiu
C 508	35	4.1	30638	2	AC020149	AC020149 Drosophi1	C 581	35	4.1	156162	2	CNS08CAN	CNS08CAN Oryza sat
C 509	35	4.1	33311	9	AC004235	AC004235 Homo sapi	C 582	35	4.1	156442	9	AC107385	AC107385 Homo sapi
C 510	35	4.1	35276	2	AC115611	AC115611 Dictyoste	C 583	35	4.1	156461	2	AC090555	AC090555 Homo sapi
C 511	35	4.1	39369	2	AC115681	AC115681 Dictyoste	C 584	35	4.1	156533	2	AC117070	AC117070 Dictyoste
C 512	35	4.1	40770	2	AC122738	AC122738 Mus muscu	C 585	35	4.1	157083	2	AC117758	AC117758 Mus muscu
C 513	35	4.1	41857	2	AC126371	AC126371 Homo sapi	C 586	35	4.1	158548	3	PFMAL3P2	PFMAL3P2 Homo sapi
C 514	35	4.1	45296	2	AC115613	AC115613 Dictyoste	C 587	35	4.1	158590	2	AC130197	AC130197 Felis cat
C 515	35	4.1	47573	3	AF030694	AF030694 Plasmodiu	C 588	35	4.1	158901	9	AC093852	AC093852 Homo sapi
C 516	35	4.1	47791	2	AC115593	AC115593 Dictyoste	C 589	35	4.1	159202	2	AC087347	AC087347 Homo sapi
C 517	35	4.1	47791	2	AC115305	AC115305 Dictyoste	C 590	35	4.1	159202	2	AC117082	AC117082 Dictyoste
C 518	35	4.1	53150	2	AC116984	AC116984 Dictyoste	C 591	35	4.1	160893	2	AC094329	AC094329 Homo sapi
C 519	35	4.1	56956	2	AC117081	AC117081 Dictyoste	C 592	35	4.1	162143	2	AC097553	AC097553 Homo sapi
C 520	35	4.1	58641	2	AC104030	AC104030 Homo sapi	C 593	35	4.1	162367	2	AC103241	AC103241 Dictyoste
C 521	35	4.1	58641	2	AC104030	AC104030 Homo sapi	C 594	35	4.1	162643	2	AC113327	AC113327 Mus muscu
C 522	35	4.1	59004	2	AC115680	AC115680 Dictyoste	C 595	35	4.1	163166	9	AL356632	AL356632 Human DNA
C 523	35	4.1	59507	2	AC122581	AC122581 Rattus no	C 596	35	4.1	163332	2	AC115239	AC115239 Rattus no
C 524	35	4.1	60182	2	PFMAL1P6	PFMAL1P6 Plasmodiu	C 597	35	4.1	164521	2	AC119354	AC119354 Homo sapi
C 525	35	4.1	60583	8	AB011475	AB011475 Arabidops	C 598	35	4.1	164744	2	AC018914	AC018914 Homo sapi
C 526	35	4.1	61020	6	AX251546	AX251546 Sequence	C 599	35	4.1	165269	2	AC117064	AC117064 Rattus no
C 527	35	4.1	62352	2	AC116990	AC116990 Dictyoste	C 600	35	4.1	165804	2	AC016840	AC016840 Homo sapi
C 528	35	4.1	62352	2	AC116990	AC116990 Dictyoste	C 601	35	4.1	165814	2	AC102296	AC102296 Mus muscu
C 529	35	4.1	68080	2	AL169555	AL169555 Dictyoste	C 602	35	4.1	165878	2	AC073382	AC073382 Homo sapi
C 530	35	4.1	69027	9	AL596306	AL596306 Human DNA	C 603	35	4.1	166333	2	AC013749	AC013749 Homo sapi
C 531	35	4.1	69868	2	AC102302	AC102302 Mus muscu	C 604	35	4.1	166617	10	AF332859S2	AF332859S2 Mus muscu
C 532	35	4.1	71580	2	AC118250	AC118250 Homo sapi	C 605	35	4.1	166676	2	AC106845	AC106845 Homo sapi
C 533	35	4.1	74284	2	AC034277	AC034277 Homo sapi	C 606	35	4.1	169172	2	AC026663	AC026663 Homo sapi
C 534	35	4.1	74850	2	AC094412	AC094412 Rattus no	C 607	35	4.1	170844	2	AL805938	AL805938 Mus muscu
C 535	35	4.1	77096	2	AC116030	AC116030 Dictyoste	C 608	35	4.1	171187	2	AC116960	AC116960 Dictyoste
C 536	35	4.1	81179	2	AC116100	AC116100 Dictyoste	C 609	35	4.1	171681	2	AC091541	AC091541 Canis fam
C 537	35	4.1	81179	2	AC116100	AC116100 Dictyoste	C 610	35	4.1	173920	2	AC120747	AC120747 Rattus no
C 538	35	4.1	93491	2	AL16967	AL16967 Dictyoste	C 611	35	4.1	173977	2	AL845165	AL845165 Mus muscu
C 539	35	4.1	96863	2	AL591388	AL591388 Homo sapi	C 612	35	4.1	174087	2	CNS08CB7	CNS08CB7 Oryza sat
C 540	35	4.1	99670	9	AC007200	AC007200 Homo sapi	C 613	35	4.1	174418	2	AC125096	AC125096 Mus muscu
C 541	35	4.1	100726	2	AC116961	AC116961 Dictyoste	C 614	35	4.1	174851	2	AC098449	AC098449 Rattus no
C 542	35	4.1	104014	2	AC116921	AC116921 Dictyoste	C 615	35	4.1	176113	2	AL844198	AL844198 Mus muscu
C 543	35	4.1	105470	2	AL16306	AL16306 Dictyoste	C 616	35	4.1	176671	2	AC115133	AC115133 Rattus no
C 544	35	4.1	106958	9	AL807813	AL807813 Human DNA	C 617	35	4.1	177130	2	AC019351	AC019351 Homo sapi
C 545	35	4.1	107288	2	AC116923	AC116923 Dictyoste	C 618	35	4.1	180169	2	AC098961	AC098961 Rattus no
C 546	35	4.1	107686	2	AC105493	AC105493 Rattus no	C 619	35	4.1	180355	2	AC022167	AC022167 Homo sapi
C 547	35	4.1	107739	2	AC116979	AC116979 Dictyoste	C 620	35	4.1	180416	2	AC096793	AC096793 Rattus no
C 548	35	4.1	108908	3	PFMAL3P8	PFMAL3P8 Plasmodiu	C 621	35	4.1	180731	2	AC103182	AC103182 Rattus no
C 549	35	4.1	109342	2	AC095081	AC095081 Rattus no	C 622	35	4.1	181242	2	AL807820	AL807820 Mus muscu
C 550	35	4.1	110000	2	AC084053_0	AC084053 Mus muscu	C 623	35	4.1	181253	2	AC098537	AC098537 Rattus no
C 551	35	4.1	110000	2	AC096324_1	AC096324_1 Continuation (2 of	C 624	35	4.1	181335	2	AC016131	AC016131 Drosophi1
C 552	35	4.1	111187	2	AC009283	AC009283 Homo sapi	C 625	35	4.1	182431	2	AC068380	AC068380 Homo sapi
C 553	35	4.1	111492	2	AC103477	AC103477 Rattus no	C 626	35	4.1	183183	10	AC104328	AC104328 Mus muscu
C 554	35	4.1	111744	2	AC096968	AC096968 Homo sapi	C 627	35	4.1	183328	2	AC101773	AC101773 Mus muscu
C 555	35	4.1	115981	2	AL591072	AL591072 Human DNA	C 628	35	4.1	183758	10	AL645522	AL645522 Mouse DNA
C 556	35	4.1	116688	9	HSJ393E18	HSJ393E18 Dictyoste	C 629	35	4.1	183800	2	AC123118	AC123118 Rattus no
C 557	35	4.1	117314	2	AC121242	AC121242 Medicago	C 630	35	4.1	183800	2	AC123118	AC123118 Rattus no
C 558	35	4.1	119295	2	AC127427	AC127427 Magnapor	C 631	35	4.1	184865	2	AL807824	AL807824 Mus muscu
C 559	35	4.1	123280	2	AC117076	AC117076 Dictyoste	C 632	35	4.1	184909	2	AL844863	AL844863 Mus muscu
C 560	35	4.1	123830	2	AC100244	AC100244 Mus muscu	C 633	35	4.1	186162	2	AC094995	AC094995 Rattus no
C 561	35	4.1	124820	2	AC117073	AC117073 Dictyoste	C 634	35	4.1	186465	9	AC105052	AC105052 Homo sapi
C 562	35	4.1	127211	2	AC117066	AC117066 Rattus no	C 635	35	4.1	187083	10	AC117233	AC117233 Mus muscu
C 563	35	4.1	128941	2	AC110348	AC110348 Rattus no	C 636	35	4.1	188391	10	AL671400	AL671400 Mouse DNA
C 564	35	4.1	135925	2	AC128140	AC128140 Rattus no	C 637	35	4.1	188993	2	AC109656	AC109656 Rattus no
C 565	35	4.1	136607	9	AC083809	AC083809 Homo sapi	C 638	35	4.1	189123	3	AC093998	AC093998 Rattus no
C 566	35	4.1	137410	2	AC113861	AC113861 Rattus no	C 639	35	4.1	190225	9	AC023383	AC023383 Homo sapi
C 567	35	4.1	140576	2	AC120524	AC120524 Felis cat	C 640	35	4.1	190984	9	AC018781	AC018781 Homo sapi
C 568	35	4.1	140855	2	AC094340	AC094340 Rattus no	C 641	35	4.1	191385	2	AC025283	AC025283 Homo sapi
C 569	35	4.1	140855	2	AC094340	AC094340 Rattus no	C 642	35	4.1	192309	2	AC115642	AC115642 Rattus no
C 570	35	4.1	141358	2	AC097196	AC097196 Rattus no	C 643	35	4.1	192929	2	AC005505	AC005505 Plasmodiu
C 571	35	4.1	146255	2	AC084170	AC084170 Homo sapi	C 644	35	4.1	193149	2	AC123256	AC123256 Rattus no
C 572	35	4.1	149253	2	AC012245	AC012245 Homo sapi	C 645	35	4.1	193383	2	AC123256	AC123256 Rattus no
C 573	35	4.1	150060	2	AC108973	AC108973 Rattus no	C 646	35	4.1	194907	2	AC106835	AC106835 Mus muscu
C 574	35	4.1	150759	2	AP001130	AP001130 Homo sapi	C 647	35	4.1	195411	10	AL669958	AL669958 Mouse DNA
C 575	35	4.1	151736	2	AC024439	AC024439 Homo sapi	C 648	35	4.1	195411	10	AL669958	AL669958 Mouse DNA
C 576	35	4.1	152506	2	AC100830	AC100830 Homo sapi	C 649	35	4.1	198088	9	AC078957	AC078957 Homo sapi

C 650	35	4.1 198273	2	AC107366	Mus muscu	C 723	34	3.9	130	6	AX256038	AX256038 Sequence
C 651	35	4.1 199551	2	AC006281	Plasmodiu	724	34	3.9	161	6	A08916	A08916 H.sapiens (
C 652	35	4.1 199960	2	AC108944	Mus muscu	725	34	3.9	210	4	AF250317	AF250317 Capsi fam
C 653	35	4.1 200789	2	AC106109	Rattus no	C 726	34	3.9	254	6	AX334011	AX334011 Sequence
C 654	35	4.1 201724	2	AC119506	Rattus no	C 727	34	3.9	254	6	AX337543	AX337543 Sequence
C 655	35	4.1 202374	10	AC122868	Mus muscu	728	34	3.9	289	6	AR068753	AR068753 Sequence
C 656	35	4.1 202727	2	AC109724	Rattus no	729	34	3.9	289	6	163077	Sequence 3
C 657	35	4.1 202740	10	AC098890	Mus muscu	730	34	3.9	291	6	AX191241	AX191241 Sequence
C 658	35	4.1 202907	2	AC123073	Mus muscu	731	34	3.9	291	6	AX395977	AX395977 Sequence
C 659	35	4.1 203519	10	AC112258	Mus muscu	732	34	3.9	301	6	AF417164	AF417164 Homo sapi
C 660	35	4.1 204096	2	AC027704	Hom sapi	733	34	3.9	317	9	AK000656	AK000656 Homo sapi
C 661	35	4.1 204652	2	PFMAL13P6	Plasmodiu	734	34	3.9	324	3	AF483705	AF483705 Ixodes sc
C 662	35	4.1 205823	2	AC111087	Mus muscu	C 735	34	3.9	327	6	AX182090	AX182090 Sequence
C 663	35	4.1 206356	2	AC112085	Rattus no	C 736	34	3.9	332	6	AX186910	AX186910 Sequence
C 664	35	4.1 207392	2	AC111838	Rattus no	737	34	3.9	330	6	AX046458	AX046458 Sequence
C 665	35	4.1 207456	2	AC113025	Mus muscu	738	34	3.9	374	6	AX198829	AX198829 Sequence
C 666	35	4.1 207957	9	AC004470	Homo sapi	739	34	3.9	374	6	AX209356	AX209356 Sequence
C 667	35	4.1 208160	2	AC123215	Mus muscu	740	34	3.9	381	3	AF159974	AF159974 Butus ma
C 668	35	4.1 208568	2	AC110349	Rattus no	741	34	3.9	382	9	AF207859	AF207859 Homo sapi
C 669	35	4.1 210423	2	AL672074	Mus muscu	742	34	3.9	384	3	AF483734	AF483734 Ixodes sc
C 670	35	4.1 213171	2	AC124200	Mus muscu	743	34	3.9	385	3	AF151796	AF151796 Butus ma
C 671	35	4.1 213251	2	AC116458	Mus muscu	744	34	3.9	386	3	AF495660	AF495660 Varecia v
C 672	35	4.1 213303	2	AC116458	Mus muscu	745	34	3.9	409	3	AF156597	AF156597 Butus ma
C 673	35	4.1 215115	10	AL671520	Mouse DNA	746	34	3.9	426	9	HSM802848	HSM802848 Sequence
C 674	35	4.1 216920	2	AC094599	Rattus no	747	34	3.9	427	6	AX070822	AX070822 Drosophila
C 675	35	4.1 216937	2	AC023061	Mus muscu	C 748	34	3.9	427	6	AX330416	AX330416 Sequence
C 676	35	4.1 217014	2	AC104549	Mus muscu	749	34	3.9	431	3	AF483662	AF483662 Ixodes sc
C 677	35	4.1 219519	2	AC115753	Mus muscu	750	34	3.9	446	3	AF146743	AF146743 Mesobuthu
C 678	35	4.1 221548	2	AC099714	Mus muscu	C 751	34	3.9	446	11	G21964	G21964 human SMS W
C 679	35	4.1 222618	2	AC110335	Rattus no	C 752	34	3.9	452	11	G24486	G24486 human SMS W
C 680	35	4.1 224149	2	AC119799	Pan trogl	C 753	34	3.9	457	11	G24145	G24145 human SMS W
C 681	35	4.1 225204	2	AL772138	Mus muscu	754	34	3.9	458	6	AR105608	AR105608 Sequence
C 682	35	4.1 227617	2	AC125352	Mus muscu	755	34	3.9	458	6	AR105608	AR105608 Sequence
C 683	35	4.1 228023	2	AL672184	Mus muscu	C 756	34	3.9	458	11	G27046	G27046 human SMS S
C 684	35	4.1 228793	2	AC107719	Mus muscu	C 757	34	3.9	460	3	AY113221	AY113221 Drosophila
C 685	35	4.1 229793	2	AC019272	Homo sapi	C 758	34	3.9	463	8	AF333788	AF333788 Pinus tae
C 686	35	4.1 230629	2	AC019272	Homo sapi	C 759	34	3.9	463	8	BC007974	BC007974 Homo sapi
C 687	35	4.1 240065	2	AC093481	Mus muscu	C 760	34	3.9	475	6	AI4236	AI4236 D5 anonymu
C 688	35	4.1 240864	2	AC006510	Homo sapi	761	34	3.9	475	9	BC031580	BC031580 Homo sapi
C 689	35	4.1 242218	2	AC104917	Mus muscu	762	34	3.9	479	3	DDCOX6R	DDCOX6R Homo sapi
C 690	35	4.1 242835	2	AC079243	Mus muscu	763	34	3.9	490	10	AF172930	AF172930 Mus muscu
C 691	35	4.1 242979	2	AC093478	Mus muscu	764	34	3.9	493	8	NTTIMPA	NTTIMPA Homo sapi
C 692	35	4.1 253756	2	AC093975	Rattus no	765	34	3.9	506	3	AF072331	AF072331 Schistos
C 693	35	4.1 256774	2	AC115964	Diclyoste	766	34	3.9	521	10	AY028425	AY028425 Mus muscu
C 694	35	4.1 256774	2	AC115964	Diclyoste	767	34	3.9	522	9	AF417129	AF417129 Homo sapi
C 695	35	4.1 261381	2	AL596386	Mus muscu	768	34	3.9	530	9	BC022858	BC022858 Homo sapi
C 696	35	4.1 261381	2	AL596386	Mus muscu	769	34	3.9	531	8	AF140500	AF140500 Oryza sat
C 697	35	4.1 263662	2	AC114344	Rattus no	770	34	3.9	560	8	PR249397	PR249397 Phleum pr
C 698	35	4.1 263775	2	AC115418	Rattus no	771	34	3.9	561	9	IR0687685	IR0687685 Homo sapi
C 699	35	4.1 268578	2	AC094863	Rattus no	772	34	3.9	570	9	AF277181	AF277181 Homo sapi
C 700	35	4.1 271222	2	AC124770	Mus muscu	773	34	3.9	586	3	AY066029	AY066029 Branchios
C 701	35	4.1 278082	2	AC112365	Rattus no	774	34	3.9	591	3	CCMASPRRO	CCMASPRRO Ceratilis c
C 702	35	4.1 278307	2	AC118873	Rattus no	C 775	34	3.9	592	6	AX421572	AX421572 Sequence
C 703	35	4.1 280982	2	AC125184	Mus muscu	776	34	3.9	596	9	AF417145	AF417145 Homo sapi
C 704	35	4.1 287820	2	AC096329	Rattus no	777	34	3.9	602	9	BC015519	BC015519 Homo sapi
C 705	35	4.1 291545	3	AE003600	Drosophila	778	34	3.9	607	5	AF321772	AF321772 Ophiophag
C 706	35	4.1 293431	2	PFMAL13P4	Plasmodiu	779	34	3.9	610	8	AB047923	AB047923 Oryza sat
C 707	35	4.1 308692	2	AC098559	Rattus no	780	34	3.9	611	6	AX187051	AX187051 Sequence
C 708	35	4.1 309233	2	AC098557	Rattus no	781	34	3.9	611	10	BC026656	BC026656 Mus muscu
C 709	35	4.1 310779	2	AC005140	Plasmodiu	782	34	3.9	613	10	S76337	S76337 IGF-binding
C 710	35	4.1 318930	2	AC073495	Mus muscu	783	34	3.9	613	10	BC028889	BC028889 Mus muscu
C 711	35	4.1 321003	2	PFMAL4P3	Plasmodiu	784	34	3.9	625	8	AF110779	AF110779 Lilium lo
C 712	35	4.1 349980	6	AX344552	Sequence	C 785	34	3.9	631	6	AX338092	AX338092 Sequence
C 713	35	4.1 349980	6	AX344554	Sequence	786	34	3.9	633	6	AR038867	AR038867 Sequence
C 714	35	4.1 349980	6	AX344557	Sequence	787	34	3.9	655	3	AF420265	AF420265 Anopheles
C 715	35	4.1 349980	6	AX344560	Sequence	C 788	34	3.9	655	6	AX185692	AX185692 Sequence
C 716	35	4.1 349980	6	AX344563	Sequence	789	34	3.9	665	9	BC021122	BC021122 Homo sapi
C 717	35	4.1 349980	6	AX344564	Sequence	790	34	3.9	666	3	AY047580	AY047580 Drosophila
C 718	35	4.1 349980	6	AX344565	Sequence	791	34	3.9	669	9	HSM800251	HSM800251 Homo sapi
C 719	35	4.1 349980	6	AX344569	Sequence	792	34	3.9	673	8	CRP5237	CRP5237 Homo sapi
C 720	34	3.9 77	6	A08908	H.sapiens (793	34	3.9	677	9	AB055315	AB055315 Macaca fa
C 721	34	3.9 96	6	A08909	H.sapiens (794	34	3.9	677	9	BC018211	BC018211 Homo sapi
C 722	34	3.9 104	6	A08910	H.sapiens (795	34	3.9	690	9	BC021234	BC021234 Homo sapi

796	34	3-9	703	6	AX259734	Sequence	869	34	3-9	973	9	BC017067	BC017067 Homo sapi
797	34	3-9	707	8	DROCPY1	6623398 Drosophila	C 870	34	3-9	975	3	DD087514	U87514 Dictyosteli
798	34	3-9	708	8	PSGDCP	X54377 P.sativum g	871	34	3-9	978	3	AY118474	AY118474 Drosophi
799	34	3-9	709	6	AX351026	AX351026 Sequence	872	34	3-9	987	3	AY122185	AY122185 Drosophi
800	34	3-9	711	3	DVU26847	U26847 Drosophila	873	34	3-9	987	3	SCMGST	106180 Schistosoma
801	34	3-9	713	3	AY118450	AY118450 Drosophi	874	34	3-9	989	3	AY089478	AY089478 Drosophi
802	34	3-9	714	8	AF420198	AF420198 Vitis r1p	875	34	3-9	991	9	BC020915	BC020915 Homo sapi
803	34	3-9	718	8	AF401200	AF401200 Bauhinia	876	34	3-9	994	3	AY069151	AY069151 Drosophi
804	34	3-9	734	3	AY118721	AY118721 Drosophi	877	34	3-9	999	9	BC001109	BC001109 Homo sapi
805	34	3-9	739	3	AY113352	AY113352 Drosophi	878	34	3-9	1009	3	AF030628	AF030628 Plasmodi
806	34	3-9	746	6	AR137703	AR137703 Sequence	879	34	3-9	1012	9	BC009540	BC009540 Homo sapi
807	34	3-9	748	6	A21101	A21101 N.tabacum S	880	34	3-9	1012	9	BC004052	BC004052 Homo sapi
808	34	3-9	748	6	144072	144072 Sequence 3	881	34	3-9	1015	5	AB064665	AB064665 Homo sapi
809	34	3-9	749	3	HSA420433	HA420433 Homo sapi	C 882	34	3-9	1016	2	AC014440	AC014440 Drosophi
810	34	3-9	758	3	AY060876	AY060876 Drosophi	883	34	3-9	1016	2	CFMFL	X92505 C.familiar
811	34	3-9	759	3	AY118716	AY118716 Drosophi	884	34	3-9	1017	4	AY060602	AY060602 Drosophi
812	34	3-9	761	11	CNS06KKG	AL402998 t7 end of	885	34	3-9	1018	3	AY113302	AY113302 Drosophi
813	34	3-9	762	3	BC029884	BC029884 Homo sapi	886	34	3-9	1029	3	AX158283	AX158283 Sequence
814	34	3-9	769	3	ATU60981	U60981 Arabidopsis	887	34	3-9	1033	6	AF062915	AF062915 Arabidops
815	34	3-9	770	10	BC024391	BC024391 Mus muscu	888	34	3-9	1038	5	AY078168	AY078168 Dantio ter
816	34	3-9	771	8	BC000608	BC000608 Homo sapi	889	34	3-9	1049	9	BC011461	BC011461 Homo sapi
817	34	3-9	779	8	PYU63631	U63631 Fragaria x	890	34	3-9	1055	4	BTCASA1	X82401 B. taurus CA
818	34	3-9	781	9	AF237812	AF237812 Homo sapi	C 891	34	3-9	1059	10	BC025911	BC025911 Mus muscu
819	34	3-9	793	10	BC022621	BC022621 Mus muscu	892	34	3-9	1069	9	BC009520	BC009520 Homo sapi
820	34	3-9	796	6	A23630	A23630 Corn anther	893	34	3-9	1069	9	AF339776	AF339776 Homo sapi
821	34	3-9	796	6	133111	133111 Sequence 2	894	34	3-9	1071	9	DDICABP	M36174 D. discoidu
822	34	3-9	814	3	AF483742	AF483742 Ixodes sc	895	34	3-9	1074	3	STPBPCEN	X99320 S. tuberosum
823	34	3-9	815	9	HSA406952	HA406952 Homo sapi	896	34	3-9	1089	8	DV4A	X15381 Dictyosteli
824	34	3-9	817	3	AF132912	AF132912 Drosophi	897	34	3-9	1091	3	AY070897	AY070897 Homo sapi
825	34	3-9	818	9	BC032631	BC032631 Homo sapi	898	34	3-9	1092	3	AF237620	AF237620 Mus muscu
826	34	3-9	820	10	BC033606	BC033606 Homo sapi	899	34	3-9	1096	3	AY118489	AY118489 Mus muscu
827	34	3-9	829	9	AF339780	AF339780 Mus muscu	900	34	3-9	1096	3	AY118489	BC032362 Homo sapi
828	34	3-9	830	8	AF303940	AF303940 Glycine m	901	34	3-9	1096	10	BC032962	BC032962 Homo sapi
829	34	3-9	835	10	AF260436	AF260436 Rattus no	902	34	3-9	1098	8	BOWIPATCP	X95639 B. oleracea
830	34	3-9	836	9	BC013035	BC013035 Homo sapi	903	34	3-9	1104	8	AY078282	AY078282 Thalassio
831	34	3-9	837	8	NPSODM	X55974 N.plumbagin	904	34	3-9	1105	8	AY078282	BC000777 Homo sapi
832	34	3-9	840	9	BC006414	BC006414 Homo sapi	905	34	3-9	1107	9	BC006305	BC006305 Homo sapi
833	34	3-9	843	4	AF319463	AF319463 Macropus	906	34	3-9	1110	5	AF143806	AF143806 Gallus ga
834	34	3-9	845	3	AF047612	AF047612 Euroglyph	907	34	3-9	1111	5	AF143806	BC000853 Homo sapi
835	34	3-9	852	3	AY118642	AY118642 Drosophi	908	34	3-9	1111	5	AF143806	AY119480 Drosophi
836	34	3-9	852	3	SSEPDIINH	X96361 S.pombe SPD	909	34	3-9	1115	5	AR460212	AR460212 Crocodylu
837	34	3-9	853	8	CPCRMA	Y08240 C.pteroides	910	34	3-9	1115	5	AR460212	BC032317 Homo sapi
838	34	3-9	857	10	BC023139	BC023139 Mus muscu	911	34	3-9	1116	5	BC032317	BC012595 Homo sapi
839	34	3-9	864	9	HSCBCIP1	Y10776 H.sapiens m	912	34	3-9	1118	9	AY119027	AY119027 Drosophi
840	34	3-9	871	3	AY089389	AY089389 Drosophi	913	34	3-9	1128	3	AX244574	AX244574 Sequence
841	34	3-9	875	9	BC030260	BC030260 Homo sapi	914	34	3-9	1128	3	AF274025	AF274025 Homo sapi
842	34	3-9	876	8	AF286464	AF286464 Potereesi	915	34	3-9	1129	9	BC032768	BC032768 Homo sapi
843	34	3-9	879	9	BC007021	BC007021 Homo sapi	916	34	3-9	1129	9	BC032768	AY118699 Drosophi
844	34	3-9	888	9	BC016970	BC016970 Homo sapi	917	34	3-9	1130	6	AX033386	AX033386 Sequence
845	34	3-9	899	9	AF368271	AF368271 Homo sapi	918	34	3-9	1131	6	AX033386	AF271660 Vitis ber
846	34	3-9	900	6	AR105095	AR105095 Sequence	919	34	3-9	1133	8	AF529691	AF529691 Brassica
847	34	3-9	900	8	AF141879	AF141879 Oryza sat	920	34	3-9	1133	8	AF529691	AF116670 Homo sapi
848	34	3-9	900	8	AF244699	AF244699 Zea mays	921	34	3-9	1133	8	AF529691	E01349
849	34	3-9	903	8	AY118755	AY118755 Drosophi	922	34	3-9	1134	17	AF116670	E01349
850	34	3-9	905	3	BC015507	BC015507 Homo sapi	923	34	3-9	1136	6	E01349	I08009
851	34	3-9	907	3	AY118472	AY118472 Drosophi	924	34	3-9	1142	3	AY089349	AY089349 Drosophi
852	34	3-9	910	3	BC014198	BC014198 Homo sapi	925	34	3-9	1142	3	AY089349	BC007389 Homo sapi
853	34	3-9	913	3	AY118492	AY118492 Drosophi	926	34	3-9	1143	6	AR122651	AR122651 Sequence
854	34	3-9	918	8	AF017363	AF017363 Oryza sat	927	34	3-9	1146	6	AR122651	BC009016 Homo sapi
855	34	3-9	929	9	D82059	D82059 Homo sapien	928	34	3-9	1147	9	BC009016	X74732 A.hypochoind
856	34	3-9	930	10	BC028754	BC028754 Mus muscu	929	34	3-9	1152	8	AHLHAH	AR094308 Sequence
857	34	3-9	945	5	HSW801971	AY040528 Gallus ga	930	34	3-9	1154	6	AR094308	BC032114 Homo sapi
858	34	3-9	948	5	AY040528	AF320777 Homo sapi	931	34	3-9	1156	9	BC032114	AF331040 Mus muscu
859	34	3-9	951	6	AF320777	AX052820 Sequence	932	34	3-9	1159	10	AF331040	AF460211 Crocodylu
860	34	3-9	959	6	AX052820	X61970 H.sapiens m	933	34	3-9	1161	8	MNRHBCSA	M95930 Mantho esc
861	34	3-9	959	9	HSMPEZE	X65700 N.tabacum m	934	34	3-9	1168	10	BC019114	BC019114 Mus muscu
862	34	3-9	961	8	NTAP24	BC027572 Mus muscu	935	34	3-9	1173	10	BC014724	U48706 Dictyostell
863	34	3-9	962	10	BC027572	BC034133 Mus muscu	936	34	3-9	1182	3	DDU48706	M931009 Human L-iso
864	34	3-9	962	10	BC034133	AY119476 Drosophi	937	34	3-9	1182	3	HUMIZOI	AX275042 Sequence
865	34	3-9	965	10	AY119476	AF106945 Rattus no	938	34	3-9	1190	6	AX275042	AY118797 Drosophi
866	34	3-9	965	10	AF106945	AF144430 Lygus 1in	939	34	3-9	1191	3	AY118797	
867	34	3-9	971	10	AF144430	BC030946 Mus muscu	940	34	3-9				
868	34	3-9	971	10	BC030946		941	34	3-9				

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Run on: February 8, 2003, 08:37:15 : Search time 234 Seconds
(without alignments)
8305.447 Million cell updates/sec

Title: US-10-021-811-35
Perfect score: 863
Sequence: 1 gccacgagctctacacacac.....aaaaaaaaaaaaaaaa 863

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : N_Geneseq_101002:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	4.8	2037	24	AAD24013 Human drug metabol
2	41	4.8	2307	19	AAV44318 Mize search-associ
3	41	4.8	4329	19	AAV44319 Seq ID #7 from DB1
4	40	4.6	10825	24	ABN80207 Human chemically m
5	39	4.5	398	22	AA188050 Human polynucleoti
6	39	4.5	1061	24	ABO21136 Oligonucleotide fo
7	39	4.5	1061	24	ABO21137 Oligonucleotide fo
8	39	4.5	1402	22	AA157850 Human polynucleoti
9	39	4.5	3001	24	ABN80333 Human chemically m

C 10	39	4.5	5273	24	ABL32875 Human immune syste
C 11	39	4.5	5313	24	ABL32763 Human immune syste
C 12	39	4.5	6120	24	ABN80302 Human chemically m
C 13	39	4.5	6120	24	ABK28439 DNA transcription
C 14	39	4.5	6956	24	ABL70225 Chemically treated
C 15	39	4.5	7046	24	ABN80288 Human chemically m
C 16	39	4.5	7046	24	ABL34116 Human immune syste
C 17	39	4.5	7890	24	ABL70240 Chemically treated
C 18	39	4.5	7890	24	AA561185 Human gene regulat
C 19	39	4.5	8246	24	ABL32203 Human immune syste
C 20	39	4.5	8372	22	AA546353 Tumour suppressor
C 21	39	4.5	9963	24	ABL32694 Human immune syste
C 22	39	4.5	11178	24	ABL70507 Chemically treated
C 23	39	4.5	11178	24	AA561059 Human gene regulat
C 24	39	4.5	11178	24	ABK31172 Signal transductio
C 25	39	4.5	13427	24	ABL33926 Human immune syste
C 26	39	4.5	15500	22	AA546508 Tumour suppressor
C 27	39	4.5	17234	24	ABO67018 Human angiogenesis
C 28	39	4.5	17389	24	ABL33414 Human immune syste
C 29	38	4.4	379	22	ABL20476 Human breast cance
C 30	38	4.4	5447	22	AA546757 Tumour suppressor
C 31	38	4.4	9770	24	ABL32032 Human immune syste
C 32	38	4.4	19798	22	AAF83671 Nucleic acid seque
C 33	38	4.4	19912	22	AAF83670 Nucleic acid seque
C 34	38	4.4	20160	22	AAF83672 Nucleic acid seque
C 35	38	4.4	20217	22	AAF83674 Nucleic acid seque
C 36	38	4.4	20247	22	AAF83675 Nucleic acid seque
C 37	38	4.4	20316	22	AAF83673 Nucleic acid seque
C 38	38	4.4	27960	22	AAK69779 Human immune/haema
C 39	38	4.4	27960	22	AAK73320 Human immune/haema
C 40	37	4.3	1137	18	AA63234 Human ubiqutin co
C 41	37	4.3	1159	22	AAF79920 Nucleotide sequenc
C 42	37	4.3	1856	18	AA63233 Human ubiqutin co
C 43	37	4.3	1856	18	ABO60785 Human UB211 cDNA s
C 44	37	4.3	3964	19	AAV62673 Tumour necrosis fa
C 45	37	4.3	4051	19	AAV62672 Sequence encoding
C 46	37	4.3	5108	14	AAO53403 Kinechohre protei
C 47	37	4.3	10136	17	AA634578 Tumour suppressor
C 48	37	4.3	56153	22	AA546794 Human nervous syst
C 49	36	4.2	152	22	ABAI17042 Human pancreatic r
C 50	36	4.2	152	22	AAAD16670 Genomic sequence #
C 51	36	4.2	152	22	AA529169 Human reproductive
C 52	36	4.2	152	22	AAK89972 Human digestive sy
C 53	36	4.2	152	22	AAI62628 Human breast or ov
C 54	36	4.2	237	23	ABV07534 Human prostate exp
C 55	36	4.2	237	23	ABV59128 Human prostate exp
C 56	36	4.2	257	23	ABV58043 Human prostate exp
C 57	36	4.2	305	23	AAH71523 Human cervical can
C 58	36	4.2	332	22	ABR06391 Human cDNA SRQ ID
C 59	36	4.2	401	22	AA8187701 Human polynucleoti
C 60	36	4.2	491	22	AA187701 Human prostate exp
C 61	36	4.2	528	23	ABV58464 Human colon cancer
C 62	36	4.2	572	21	AAZ80560 cDNA clone APPLR.
C 63	36	4.2	880	21	AAK61917 Human immune/haema
C 64	36	4.2	1007	18	AA792823 Flea saliva protei
C 65	36	4.2	1007	18	AA792823 Flea saliva protei
C 66	36	4.2	1037	19	AAV73412 Human colon cancer
C 67	36	4.2	1037	19	AAH34174 Human secreted pro
C 68	36	4.2	1131	21	AAAC93387 Lung cancer associ
C 69	36	4.2	1230	21	AAFI18268 Human polynucleoti
C 70	36	4.2	1254	24	AB189756 Human cancer cell
C 71	36	4.2	1384	24	AA144826 Human cancer cell
C 72	36	4.2	1384	24	AA144827 Human secreted pro
C 73	36	4.2	1542	22	AAO20640 Mec-4 gene. Caeno
C 74	36	4.2	1606	13	AAQ20640 Mec-4 gene. Caeno
C 75	36	4.2	1607	21	AAQ38934 Murine CIRM-2 codi
C 76	36	4.2	1626	21	AA593305 cDNA encoding nove
C 77	36	4.2	1715	20	AA541104 cDNA encoding a f
C 78	36	4.2	1736	20	AA586293 Complement of cDNA
C 79	36	4.2	1736	20	AA586293 Flea epoxide hydro
C 80	36	4.2	1736	22	AA166761 Flea epoxide hydro
C 81	36	4.2	1736	22	AA166761 Flea epoxide hydro
C 82	36	4.2	1736	22	AAAC91978 Flea epoxide hydro

C	83	36	4.2	1736	22	AAC91979	Flea epoxide hydro
C	84	36	4.2	1736	22	AAC86292	Flea epoxide hydro
C	85	36	4.2	1736	22	AAC86293	Flea epoxide hydro
C	86	36	4.2	2070	21	AAC76167	Human ORFX ORF1722
C	87	36	4.2	2325	21	AAD08296	Human secreted pro
C	88	36	4.2	2422	21	AAC76970	Human ORFX ORF2525
C	89	36	4.2	2524	21	AAC77206	Human ORFX ORF2761
C	90	36	4.2	3989	22	AAH34823	Human colon cancer
C	91	36	4.2	5750	22	AAH346708	Tumour suppressor
C	92	36	4.2	5750	24	ABL34008	Human immune syste
C	93	36	4.2	5829	24	ABL33726	Human immune syste
C	94	36	4.2	6887	24	ABN80015	Human chemically m
C	95	36	4.2	8392	24	ABL33490	Human immune syste
C	96	36	4.2	9731	24	ABL32990	Human immune syste
C	97	35	4.1	177	23	ABV6957	Human prostate exp
C	98	35	4.1	239	22	AAH33958	Human colon cancer
C	99	35	4.1	256	23	ABV6818	Human prostate exp
C	100	35	4.1	264	24	ABV07703	Human prostate exp
C	101	35	4.1	278	22	AAH69999	Human ovarian can
C	102	35	4.1	301	23	ABV19472	Human prostate exp
C	103	35	4.1	307	23	ABL87642	Human prostate exp
C	104	35	4.1	314	24	ABL63852	Breast cancer rela
C	105	35	4.1	314	23	ABV66059	Human prostate exp
C	106	35	4.1	335	22	AAI19579	Human breast cance
C	107	35	4.1	341	23	ABV18579	Human prostate exp
C	108	35	4.1	345	23	ABV07703	Human prostate exp
C	109	35	4.1	348	22	AAI90986	Human polynucleoti
C	110	35	4.1	355	24	ABV181624	Human polynucleoti
C	111	35	4.1	370	23	ABV13480	Human prostate can
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C	113	35	4.1	383	22	AAI92810	Human polynucleoti
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C	118	35	4.1	387	22	ABV57769	Human prostate exp
C	119	35	4.1	389	23	AAI88648	Human polynucleoti
C	120	35	4.1	394	23	ABV57930	Human prostate exp
C	121	35	4.1	401	22	AAI90914	Human polynucleoti
C	122	35	4.1	406	22	AAI82944	Human polynucleoti
C	123	35	4.1	406	22	AAI87091	Human polynucleoti
C	124	35	4.1	408	22	AAI89257	Human polynucleoti
C	125	35	4.1	408	22	AAI91282	Human polynucleoti
C	126	35	4.1	409	22	AAI81946	Human polynucleoti
C	127	35	4.1	412	22	AAI87923	Human polynucleoti
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C	129	35	4.1	415	22	AAI92174	Human polynucleoti
C	130	35	4.1	430	22	AAI86288	Human polynucleoti
C	131	35	4.1	434	22	AAI82908	Human polynucleoti
C	132	35	4.1	440	23	ABV42126	Human prostate exp
C	133	35	4.1	442	23	ABV46394	Human prostate exp
C	134	35	4.1	443	23	ABV48362	Human prostate exp
C	135	35	4.1	449	23	ABV48812	Human prostate exp
C	136	35	4.1	451	22	AAK88891	Human prostate exp
C	137	35	4.1	451	22	AAI57612	Human digestive sy
C	138	35	4.1	469	23	ABV56638	Human colorectal c
C	139	35	4.1	478	22	AAI87372	Human prostate exp
C	140	35	4.1	499	21	AAAC59599	Human polynucleoti
C	141	35	4.1	499	22	AAI93507	Human secreted pro
C	142	35	4.1	509	22	AAAD06268	Domestic mite Bt5
C	143	35	4.1	509	24	AAH30715	Human colon cancer
C	144	35	4.1	521	22	AAH34685	Human colon cancer
C	145	35	4.1	540	23	ABV58372	Human prostate exp
C	146	35	4.1	570	17	AAAT30258	Human prostate exp
C	147	35	4.1	570	17	AAAT30448	Cotton fibre speci
C	148	35	4.1	570	18	AAAT70048	Cotton fibre speci
C	149	35	4.1	609	18	AAAT6217	Cotton fibre speci
C	150	35	4.1	609	21	AAH35552	cDNA sequence a co
C	151	35	4.1	610	24	ABQ25734	Oligonucleotide fo
C	152	35	4.1	611	24	ABQ25735	Oligonucleotide fo
C	153	35	4.1	611	23	ABV56623	Human prostate exp
C	154	35	4.1	724	24	ABQ43744	Oligonucleotide fo
C	155	35	4.1	724	24	ABQ43745	Oligonucleotide fo

C 229	35	4.1	8964	24	ABK31373	Signal transductio	C 302	34	3.9	323	22	AAI23920	Human breast cance
230	35	4.1	10957	24	ABL33110	Human immune syste	C 303	34	3.9	327	22	AAI23920	Human breast cance
C 231	35	4.1	11523	22	AA545467	Chemically pretrea	C 304	34	3.9	332	22	AA507726	Cervical cancer pr
C 232	35	4.1	11523	22	AA546641	Tumour suppressor	305	34	3.9	337	23	ABV58905	Human cervical can
C 233	35	4.1	11523	24	ABK34001	Human DNA for stre	306	34	3.9	337	23	ABV58905	Human prostate exp
C 234	35	4.1	11523	24	ABK33922	Human immune syste	C 307	34	3.9	339	23	ABV54338	Human prostate exp
C 235	35	4.1	11523	24	ABK28323	DNA transcription	308	34	3.9	340	22	AAI93761	Human prostate exp
C 236	35	4.1	12601	24	ABL34206	Human immune syste	309	34	3.9	343	22	AAI93761	Human prostate exp
C 237	35	4.1	12601	24	ABL33999	Human immune syste	310	34	3.9	344	22	AAI88988	Human prostate exp
C 238	35	4.1	61020	22	AA546788	Tumour suppressor	311	34	3.9	344	22	AAI85033	Human prostate exp
C 239	34	3.9	77	22	AA529173	Genomic sequence #	C 312	34	3.9	345	24	ABQ85902	Human prostate exp
240	34	3.9	77	22	AAK7876	Human immune/haema	313	34	3.9	346	22	AAI87279	Human prostate exp
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243	34	3.9	82	24	AAK84669	Human immune/haema	316	34	3.9	359	21	AAA40513	Murine adult bone
C 244	34	3.9	82	24	ABN73418	Bovine embryonic g	C 317	34	3.9	359	24	ABQ85688	Arabidopsis thalia
C 245	34	3.9	90	12	AAO11762	Self-complementary	318	34	3.9	360	23	ABV59054	Human prostate exp
C 246	34	3.9	130	22	AA56585	Human CDNA for an	C 319	34	3.9	363	23	ABV12992	Human prostate exp
C 247	34	3.9	139	22	AAI25951	Human breast cance	320	34	3.9	364	23	ABV48789	Human prostate exp
C 248	34	3.9	141	16	AAI06012	Immunodominant fra	321	34	3.9	365	22	AAI83450	Human prostate exp
C 249	34	3.9	143	23	ABV19092	Human prostate exp	C 322	34	3.9	365	24	ABQ57966	Human prostate exp
250	34	3.9	156	22	AAK63711	Human immune/haema	323	34	3.9	365	18	AAI88086	Human prostate exp
251	34	3.9	159	22	AAK56708	Human immune/haema	C 324	34	3.9	369	18	AAV02169	Human prostate exp
252	34	3.9	160	23	ABV48759	Human prostate exp	325	34	3.9	370	21	AAZ51574	Haematobia irritan
253	34	3.9	171	23	ABV57330	Human prostate exp	326	34	3.9	372	21	AAI91018	Human polynucleoti
C 254	34	3.9	174	23	ABV37373	Human prostate exp	327	34	3.9	372	22	AAI83172	Human polynucleoti
C 255	34	3.9	174	24	ABL67899	Human ovarian can	328	34	3.9	373	22	AAI83172	Human polynucleoti
C 256	34	3.9	177	23	ABV5931	Human prostate exp	329	34	3.9	374	22	AA525015	Human ovarian PCR
257	34	3.9	181	23	ABV54276	Human prostate exp	330	34	3.9	374	22	AAH83660	Human ovarian tumo
258	34	3.9	190	22	AAI08206	Human breast cance	331	34	3.9	375	22	AAI90861	Human polynucleoti
259	34	3.9	191	17	AAI13475	Capture probe for	C 332	34	3.9	375	23	ABV15130	Human prostate exp
260	34	3.9	200	23	ABV19076	Human prostate exp	333	34	3.9	375	23	ABV58452	Human prostate exp
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263	34	3.9	202	22	AAK79575	Human immune/haema	336	34	3.9	378	22	AAI90863	Human polynucleoti
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266	34	3.9	206	23	ABL6453	Human prostate exp	339	34	3.9	382	23	ABV56122	Human prostate exp
C 267	34	3.9	209	23	ABV07955	Human prostate exp	340	34	3.9	383	23	ABV57015	Human prostate exp
268	34	3.9	212	23	ABV57286	Human prostate exp	341	34	3.9	384	22	AAI85450	Human polynucleoti
269	34	3.9	227	23	ABV59030	Human prostate exp	342	34	3.9	384	22	AAI88641	Human polynucleoti
270	34	3.9	227	23	ABV20080	Human prostate exp	C 343	34	3.9	385	22	AAI13572	Human polynucleoti
271	34	3.9	229	23	ABV57683	Human prostate exp	344	34	3.9	388	22	AAI87805	Human polynucleoti
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273	34	3.9	232	23	ABV58523	Human prostate exp	C 346	34	3.9	389	22	ABV10587	Human prostate exp
274	34	3.9	236	23	ABV56953	Human prostate exp	347	34	3.9	389	22	AAI88025	Human polynucleoti
275	34	3.9	239	22	ABAI1191	Human nervous syst	348	34	3.9	389	22	AAI91234	Human polynucleoti
276	34	3.9	240	23	ABV58851	Human prostate exp	349	34	3.9	390	22	AAI86998	Human polynucleoti
277	34	3.9	251	22	AAK88384	Human digestive sy	350	34	3.9	391	22	AAI87310	Human polynucleoti
278	34	3.9	251	22	AAI57596	Human colorectal c	351	34	3.9	393	22	AAI87824	Human polynucleoti
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280	34	3.9	254	24	ABL66183	Lung cancer relate	353	34	3.9	394	22	AAI87163	Human prostate exp
C 281	34	3.9	254	24	ABL66183	Prostate cancer re	C 354	34	3.9	398	23	ABV34113	Human prostate exp
C 282	34	3.9	268	23	ABV38724	Human prostate exp	C 355	34	3.9	398	23	ABV42975	Human prostate exp
C 283	34	3.9	272	23	AAI12612	Human breast cance	356	34	3.9	400	22	AAI82922	Human polynucleoti
284	34	3.9	274	23	ABV58263	Human prostate exp	357	34	3.9	400	22	AAI87341	Human polynucleoti
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C 297	34	3.9	310	24	ABL87211	Human ovarian can	370	34	3.9	413	22	AAI89034	Human polynucleoti
C 298	34	3.9	311	24	ABL87180	Human ovarian can	371	34	3.9	415	22	AAI85235	Human polynucleoti
299	34	3.9	312	22	AAK57869	Human immune/haema	372	34	3.9	415	22	AAI92380	Human polynucleoti
300	34	3.9	314	22	ABV58492	Human prostate exp	373	34	3.9	416	22	AAI87599	Human polynucleoti
C 301	34	3.9	321	21	AAA70159	Plasmodium falcipa	374	34	3.9	418	22	AAI83742	Human polynucleoti

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376	34	3.9	418	23	ABV49108	Human prostate exp	C 449	34	3.9	556	24	ABO36996	Oligonucleotide fo
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380	34	3.9	422	22	ABAI3982	Human nervous syst	C 453	34	3.9	572	24	AB146689	B tropicalis aller
381	34	3.9	423	22	AA182334	Human polynucleoti	C 454	34	3.9	592	24	AB101467	Murine apoptosis r
382	34	3.9	423	22	AA188083	Human polynucleoti	C 455	34	3.9	593	23	ABV04700	Human prostate exp
383	34	3.9	425	22	AAH34746	Human colon cancer	C 456	34	3.9	599	24	ABO66406	Arabidopsis thalia
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385	34	3.9	426	22	AA183998	Human polynucleoti	C 458	34	3.9	600	24	ABO52494	Oligonucleotide fo
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387	34	3.9	427	23	ABV31757	Human prostate exp	C 460	34	3.9	604	20	AAO52495	Oligonucleotide fo
388	34	3.9	427	23	AB162588	Colon adenocarcino	C 461	34	3.9	604	21	AAO52495	Oligonucleotide fo
389	34	3.9	428	22	AA185047	Human polynucleoti	C 462	34	3.9	604	21	AAO52495	Oligonucleotide fo
390	34	3.9	431	22	AA183653	Human polynucleoti	C 463	34	3.9	608	21	AAO52495	Oligonucleotide fo
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421	34	3.9	478	22	AA193637	Human breast cance	C 494	34	3.9	612	22	AAH71747	Arabidopsis thalia
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435	34	3.9	511	20	AA24402	Human prostate exp	C 508	34	3.9	612	22	AAH71747	Arabidopsis thalia
436	34	3.9	520	23	ABV54298	Human prostate exp	C 509	34	3.9	612	22	AAH71747	Arabidopsis thalia
437	34	3.9	521	23	ABV60727	Human prostate exp	C 510	34	3.9	612	22	AAH71747	Arabidopsis thalia
438	34	3.9	521	23	ABV47378	Human prostate exp	C 511	34	3.9	612	22	AAH71747	Arabidopsis thalia
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443	34	3.9	546	24	ABO35233	CDNA encoding nove	C 516	34	3.9	612	22	AAH71747	Arabidopsis thalia
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447	34	3.9	556	23	ABV42105	Human prostate exp	C 520	34	3.9	612	22	AAH71747	Arabidopsis thalia
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667	34	3.9	1694	22	AA525837	Human cDNA encoding	740	34	3.9	2301	21	AA09021	Human pancreatic c
668	34	3.9	1696	24	AB055028	Human ovarian anti	741	34	3.9	2307	21	AA096941	DNA secreted pro
669	34	3.9	1697	21	AA077781	Human cancer assoc	742	34	3.9	2430	16	AA083161	DNA encoding malic
670	34	3.9	1709	21	AA235180	Corn delta-9 acat	743	34	3.9	2434	21	AA284602	Human secreted pro
671	34	3.9	1710	14	AA047966	Rape acyl-ACP thio	744	34	3.9	2446	22	AAAD16281	Human ubiquitin ca
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C 673	34	3.9	1710	23	ABV22936	Human prostate exp	746	34	3.9	2483	22	ABA83251	Human secreted pro
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C 678	34	3.9	1710	23	ABV28767	Human prostate exp	751	34	3.9	2518	24	ABK47452	Human secreted pro
C 679	34	3.9	1729	22	ABA06527	Human cDNA SEQ ID	752	34	3.9	2527	21	AA047398	DNA encoding human
C 680	34	3.9	1747	20	AA097979	Human secreted pro	753	34	3.9	2545	22	AA005390	Human secreted pro
C 681	34	3.9	1749	22	AA160696	Human polynucleoti	754	34	3.9	2561	21	AA075822	Human ORFX ORF137
C 682	34	3.9	1749	22	AB190045	Human polynucleoti	755	34	3.9	2576	24	ABN95640	Gene #2138 used to
C 683	34	3.9	1754	22	AA533356	DNA encoding human	756	34	3.9	2576	24	ABK50069	DNA encoding human
C 684	34	3.9	1760	21	AA059930	Human secreted pro	757	34	3.9	2576	24	AB168591	Kidney cancer rela
C 685	34	3.9	1760	21	AA243782	Human fetal brain	758	34	3.9	2581	22	AA041263	cDNA encoding nove
C 686	34	3.9	1784	21	AA233337	Human secreted pro	759	34	3.9	2653	21	AA000338	Wheat raffinose sy
C 687	34	3.9	1792	21	AA015784	Human prostate can	760	34	3.9	2665	24	AB190809	Human polynucleoti
C 688	34	3.9	1816	22	AA025489	Nucleotide sequenc	761	34	3.9	2688	22	AA126760	Human breast cance
C 689	34	3.9	1823	22	AA529041	CDNA encoding for	762	34	3.9	2694	23	ABV22598	Human prostate exp
C 690	34	3.9	1827	24	ABK88010	CDNA encoding huma	763	34	3.9	2694	23	ABV28419	Human prostate exp
C 691	34	3.9	1831	21	AA046463	Human TR-receptor	764	34	3.9	2749	21	AA061157	Human fibroblast g
C 692	34	3.9	1836	19	AA033461	Human Fas ligand	765	34	3.9	2759	21	AA021752	Human breast and o
C 693	34	3.9	1837	17	AA033852	Rat vas deferens p	766	34	3.9	2760	16	AA085425	T2 DNA-polymerase
C 694	34	3.9	1841	16	AA091311	Human Fas-L gene.	C 767	34	3.9	2760	16	AA085425	T4 DNA-polymerase
C 695	34	3.9	1841	16	AA024879	Human Fas ligand (C 768	34	3.9	2770	24	AB150577	Human OST131 polyn
C 696	34	3.9	1841	20	AA021574	Human FasL protein	769	34	3.9	2772	22	AA092074	Human PRO1277 cDNA
C 697	34	3.9	1852	21	AA077519	Human ORFX ORF3074	770	34	3.9	2773	21	AA065009	Membrane-bound pro
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C 699	34	3.9	1866	20	AA084466	Human secreted pro	772	34	3.9	2773	22	AA044155	Human PRO1277 (UNQ
C 700	34	3.9	1866	22	ABAB3249	Human secreted pro	773	34	3.9	2782	22	AB006408	Human cDNA SEQ ID
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C 702	34	3.9	1902	24	AB06106	Human mur dgtase	775	34	3.9	2795	21	AA025443	Natural killer 1yt
C 703	34	3.9	1913	21	AA059920	Human secreted pro	776	34	3.9	2823	17	AA035233	Human prostate can
C 704	34	3.9	1918	22	AA053399	Human secreted pro	777	34	3.9	2825	21	AA016237	Human prostate can
C 705	34	3.9	1934	17	AA013229	OR-1 orphan recept	778	34	3.9	2847	22	AA078271	Nucleotide sequenc
C 706	34	3.9	1946	21	AA098232	Human colon cancer	779	34	3.9	2852	24	AB073250	Human MAP kinase p
C 707	34	3.9	1963	24	AB189766	Human polynucleoti	780	34	3.9	2880	20	AA087477	Rat capsaicin rece
C 708	34	3.9	1964	22	AA015328	Human cDNA sequenc	781	34	3.9	2922	21	AA019729	Human secreted pro
C 709	34	3.9	1971	20	AA008428	Acidic leucine am	782	34	3.9	2922	21	AA016664	Human secreted pro
C 710	34	3.9	1976	23	AB022114	Human prostate exp	783	34	3.9	2930	22	AA072750	Human prostate can
C 711	34	3.9	1978	14	AA037189	Petunia BPS synth	784	34	3.9	2964	24	AA088022	Cucumber LipoX DNA
C 712	34	3.9	1999	23	AB128468	Drosophila melanog	785	34	3.9	3094	22	AB190658	Human polynucleoti
C 713	34	3.9	2021	24	AB054639	Human ovarian anti	786	34	3.9	3121	21	AA094131	Haemopoietic ste
C 714	34	3.9	2030	20	AA023135	Wheat sucrose tran	787	34	3.9	3213	20	AA059631	Human adipose tiss
C 715	34	3.9	2034	22	AA006011	Human neuronal apo	788	34	3.9	3213	24	AA055742	Human secreted pro
C 716	34	3.9	2060	24	AA033348	Human consensus se	789	34	3.9	3220	21	AB092068	Human polynucleoti
C 717	34	3.9	2092	24	AB190358	Human secreted pro	790	34	3.9	3220	21	AA028457	Human D-SLAM cDNA.
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C 719	34	3.9	2106	22	AA033397	Human colon cancer	792	34	3.9	3375	24	AB054651	CDNA encoding nove
C 720	34	3.9	2123	24	AB055071	Human ovarian anti	793	34	3.9	3504	11	AA005304	Human ovarian anti
C 721	34	3.9	2143	16	AA090242	Full length Sorghu	794	34	3.9	3522	20	AA079065	Clone Ind2 encodin
C 722	34	3.9	2159	22	AA098708	Human ovarian can	795	34	3.9	3535	21	AA051555	A.thaliana AtMH3
C 723	34	3.9	2164	21	AA075653	Human ORFX ORF1208	796	34	3.9	3586	24	AA063367	Human hypoxia resp
C 724	34	3.9	2187	21	AA029220	Human thiredoxin	797	34	3.9	3623	20	AA082821	Chemically pretrea
C 725	34	3.9	2187	22	AA005850	Human secreted pro	798	34	3.9	3623	20	AA0828356	Rabbit osteoclast
C 726	34	3.9	2187	24	AA172961	Human thiredoxin	799	34	3.9	3677	20	AA028356	Rabbit osteoclast
C 727	34	3.9	2218	20	AA084503	Human secreted pro	800	34	3.9	3715	24	ABK34012	Human DNA for stag
C 728	34	3.9	2218	22	AB083415	Human secreted pro	801	34	3.9	3715	24	ABK31544	Signal transductio
C 729	34	3.9	2230	20	AA052516	Maize diphenyl oxi	802	34	3.9	3751	20	AA024227	Human normal blad
C 730	34	3.9	2230	22	AA003556	Alternative form o	803	34	3.9	3960	20	AA055606	Human angiogenesi
C 731	34	3.9	2230	24	AB101574	Human secreted pro	804	34	3.9	3960	20	AA055606	Human clone 65 pro
C 732	34	3.9	2264	20	AA020496	Human secreted pro	805	34	3.9	3973	24	AA055607	Human clone 65 ant
C 733	34	3.9	2272	24	AA051306	Human cDNA encodin	806	34	3.9	4131	18	AA082990	Human immune syste
C 734	34	3.9	2272	24	AB066630	Human polynucleoti	807	34	3.9	4134	24	AB159964	Dogfish shark kidn
C 735	34	3.9	2298	24	AA033346	Human BSRP-Rae/Ret	808	34	3.9	4134	24	ABK14910	DNA encoding shark
C 736	34	3.9	2300	20	AA0200686	Human GPC3 DNA. H	C 809	34	3.9	4163	24	AB134330	DNA immune syste
C 737	34	3.9	2300	24	ABN97384	Gene #3882 used to	810	34	3.9	4292	21	AA021792	Human breast and o
C 738	34	3.9	2300	24	AB165225	Lung cancer relate	811	34	3.9	4302	21	AA077694	Human cancer assoc
C 739	34	3.9	2300	24	AB168613	Kidney cancer rela	C 812	34	3.9	4334	24	ABK34780	Human cDNA for nov

XX 29-NOV-2001.
FD
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PF 25-MAY-2001; 2001MO-US17150.
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XX 25-MAY-2000; 2000US-207901P.
PR 01-JUN-2000; 2000US-209893P.
PR 07-JUN-2000; 2000US-209861P.
FR 15-JUN-2000; 2000US-211825P.
FR 22-JUN-2000; 2000US-213744P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
XX Yue H., Sanjanwala MS, Baughn MR, Gandhi AR, Ring HZ, Elliott V,
PI Wella NK, Yang J, Khan FA, Rankumar J, Teng YT, Hafalia A, Lai P,
PI Nguyen DB, Yang MG, Lee EA, Tribouley CM, Patterson C, Lu Y,
PI Burford N, Ding L, Bruns CM, Kearney L, Reddy R;
XX WPL; 2002-097650/13.
DR P-PDSB; AAEL4445.
XX
PT New human drug metabolizing enzymes and polynucleotides encoding the
PT enzyme for diagnosing, preventing or treating cell proliferative,
PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT disorders -
PS
PS Claim 5; Page 154-155; 158pp; English.

The present sequence is human drug metabolizing enzyme (DME)-8 cDNA.
DME polypeptide, polynucleotide and modulators are useful for
diagnosis, treatment and prevention of autoimmune/inflammatory,
cell proliferative, developmental, endocrine, eye, metabolic,
and gastrointestinal disorders, including liver disorders.
The autoimmune/inflammatory disorders treatable include
AIDS, adult respiratory distress syndrome, Addison's disease,
allergies, anemia, asthma, atherosclerosis, osteoporosis, autoimmune
hemolytic anemia, autoimmune thyroiditis, Crohn's disease, atopic
dermatitis, diabetic mellitus, Graves' disease, glomerulonephritis,
rheumatoid arthritis, scleroderma, systemic lupus erythematosus,
systemic sclerosis, ulcerative colitis, haemodialysis and uveitis,
viral, bacterial, fungal, parasitic, protozoal, helminthic infections
and trauma, and cell proliferative disorders such as cancer, atypical

CC tubular

associated with hyperparathyroidism, pancreatic disorders such as type
 CC associated with hypoparathyroidism, including sarcoidosis, diabetes
 CC insipidus, hypogonadism, disorders associated with hypothyroidism
 CC including goitre, acute thyroiditis, Graves' disease, disorders
 CC associated with hyperparathyroidism, pancreatic disorders such as type

CC conjunc

CC hyperch

CC are useful for treating gastrointestinal disorders such as dysphagia,
 CC gastritis, peptic ulcer, cholelithiasis, cirrhosis, hepatitis,
 CC hyperbilirubinaemia, constipation, diarrhoea, jaundice, Wilson's disease
 CC thrombosis and hepatic tumours. The DME polypeptide is also useful for
 CC screening its agonist or antagonist.

XX
 XX
 XX Sequence 2037 BP; 427 A; 589 C; 582 G; 439 T; 0 other;
 XX

Query Match]

Matches

QY 823 TT

DD 1330 1A

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RESULT 2
AAV44318
ID AAV44318 standard; cDNA to mRNA; 2307 BP.
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AC AAV44318;
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DT 07-OCT-1998 (first entry)
XX
DE Maize starch-associated protein cDNA.
XX
KM Starch-associated protein; maize; starch grain; soluble;
XX transgenic plant; ss.
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OS Zea mays.
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FH Key Location/Qualifiers
FT CDS 33..1946
FT /tag= a
FT /product= "starch-associated protein"
FT /note= "no start codon given"
XX
PN DE19653176-A1.
XX
PD 25-JUN-1998.
XX
PF 19-DEC-1996; 96DE-1053176.
XX
PR 19-DEC-1996; 96DE-1053176.
XX
PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
XX
PI Emmermann M, Kossmann J;
XX
DR WPI; 1998-349465/31.
XX
P-PSDB; AAW64231.
XX
PT DNA encoding maize starch-associated protein in potatoes - and
PT corresponding protein, vectors, transgenic plants; antibody, starch,
PT etc.
XX
PS Claim 1; Page 43-46; 55pp; German.
XX
CC This sequence encodes a novel maize starch-associated protein that
CC occurs both bound to starch grains and in soluble form in plant cells.
CC Such a protein can be used to produce transgenic plants or plant cells
CC which are capable of synthesising modified starch.
XX
SQ Sequence 2307 BP; 693 A; 436 C; 555 G; 623 T; 0 other;
Query Match 4.8%; Score 41; DB 19; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 823 TTTATATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 863
DB 2201 TTTATATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2241
RESULT 3
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ID AAV44319 standard; DNA; 4329 BP.
XX
AC AAV44319;
XX
DT 07-OCT-1998 (first entry)
XX
DE Seq ID #7 from DE196533176.
XX
KM Starch-associated protein; maize; starch grain; soluble;
XX transgenic plant; ss.
XX
OS Unknown.
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XX
PN DE19653176-A1.
XX
PD 25-JUN-1998.
XX
PF 19-DEC-1996; 96DE-1053176.
XX
PR 19-DEC-1996; 96DE-1053176.
XX
PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
XX
PI Emmermann M, Kossmann J;
XX
DR WPI; 1998-349465/31.
XX
PT DNA encoding maize starch-associated protein in potatoes - and
PT corresponding protein, vectors, transgenic plants; antibody, starch,
PT etc.
XX
PS Disclosure; Page -; 55pp; German.
XX
CC This specification describes potato and maize starch-associated proteins
CC that occur both bound to starch grains and in soluble form in plant
CC cells. Such a protein can be used to produce transgenic plants or plant
CC cells which are capable of synthesising modified starch.
CC NOTE: This sequence is not described or represented in the specification
CC but is presented in the sequence listing.
XX
SQ Sequence 4329 BP; 1349 A; 791 C; 1048 G; 1141 T; 0 other;
Query Match 4.8%; Score 41; DB 19; Length 4329;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 4267 TTTATATATATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4307
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XX
AC ABN80207;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human chemically modified disease associated gene SEQ ID NO 224.
XX
KM Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KM heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KM dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KM antidiabetic; cytostatic; anticonvulsant; ds.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200200927-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07536.
XX
PR 30-JUN-2000; 2000DE-1032529.
XX
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIC-) EPICENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130908/17.
XX
PT Novel nucleic acid useful for diagnosis and therapy of diseases
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Search completed: February 8, 2003, 10:33:27
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RESULT 15
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XX
AC ABN80288;
XX
DT 15-JUL-2002 (first entry)
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DE Human chemically modified disease associated gene SEQ ID NO 305.
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KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KW antidiabetic; cytostatic; anticonvulsant; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200200927-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07536.
XX
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130908/17.
XX
PT Novel nucleic acid useful for diagnosis and therapy of diseases
PT associated with development genes such as diabetes, comprises a
PT sequence of a segment of chemically pretreated DNA of genes associated
PT with development -
XX
PS Claim 1; SEQ ID NO 305; 27bp; English.
XX
CC The invention relates to a nucleic acid (I) comprising a sequence at
CC least 18 bases in length of a segment of chemically pretreated DNA (II)
CC of genes associated with development selected from 87 genes listed in
CC the specification such as ACCPN, ADFW, or AFDI and comprising one of 350
CC sequences (ABN79984-ABN80333) or their complements. The invention is
CC useful for the diagnosis or therapy of diseases associated with
CC development genes, in particular disease related to homeobox containing
CC genes (HOX), like diabetes, cancer, apoptosis related diseases, syndromes
CC associated with congenital heart disease, epilepsy, diseases related to
CC histone deacetylation, Currarino syndrome, diseases related with the
CC development of the brain and limb girdle muscular dystrophy and dwarfism.
CC Oligomers specific to each of the genes are useful for detecting the
CC methylation state of all CpG dinucleotides within the 350 sequences or
CC (II) and their complementary sequences, as primer oligonucleotides for
CC the amplification of the 350 sequences, (II) and/or their complements and
CC as oligomer probes for detecting the cytosine methylation state and/or
CC single nucleotide polymorphisms (SNPs).
CC Note: The sequence data for this patent did not form part of the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.
XX
SQ Sequence 7046 BP; 1785 A; 127 C; 1669 G; 3465 T; 0 other;

Query Match 4.5%; Score 39; DB 24; Length 7046;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 825 TATATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 863
DB 2425 TATATTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2387

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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 15338381 residues

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	37	4.3	10136	5	PCR-US95-16216-2
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12	36	4.2	1736	3	US-09-471-528-22
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14	36	4.2	1736	4	US-09-634-530-22
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156	33	3.8	740	4	US-09-211-710-8	Sequence 8, Appl1	229	33	3.8	1192	3	US-09-248-335-27	Sequence 27, Appl1
157	33	3.8	740	4	US-09-615-192A-8	Sequence 8, Appl1	230	33	3.8	1212	4	US-09-182-145-35	Sequence 34, Appl1
158	33	3.8	741	2	US-08-975-316-58	Sequence 58, Appl1	231	33	3.8	1212	4	US-09-182-145-35	Sequence 35, Appl1
159	33	3.8	741	2	US-09-615-192A-58	Sequence 58, Appl1	232	33	3.8	1223	3	US-09-154-874-4	Sequence 4, Appl1
160	33	3.8	788	4	US-09-615-192A-96	Sequence 96, Appl1	233	33	3.8	1229	1	US-08-440-861-1	Sequence 1, Appl1
161	33	3.8	790	4	US-09-363-970-4	Sequence 4, Appl1	234	33	3.8	1229	1	US-08-433-854-1	Sequence 1, Appl1
162	33	3.8	812	4	US-09-091-037-7	Sequence 7, Appl1	235	33	3.8	1229	2	US-08-174-745A-1	Sequence 1, Appl1
163	33	3.8	826	4	US-09-227-357-102	Sequence 102, Appl	236	33	3.8	1229	2	US-08-195-947-1	Sequence 1, Appl1
164	33	3.8	827	5	PCT-US95-06406A-20	Sequence 20, Appl	237	33	3.8	1229	2	US-08-433-885-1	Sequence 1, Appl1
165	33	3.8	836	4	US-09-352-990-7	Sequence 7, Appl1	238	33	3.8	1229	2	US-08-433-885-1	Sequence 1, Appl1
166	33	3.8	857	4	US-09-443-184-39	Sequence 39, Appl1	239	33	3.8	1229	4	US-08-410-614-1	Sequence 1, Appl1
167	33	3.8	857	4	US-08-460-040-1	Sequence 1, Appl1	240	33	3.8	1242	4	US-08-413-974-1	Sequence 1, Appl1
168	33	3.8	911	2	US-08-924-759-9	Sequence 9, Appl1	241	33	3.8	1242	4	US-08-434-418-1	Sequence 1, Appl1
169	33	3.8	911	2	US-09-248-335-9	Sequence 9, Appl1	242	33	3.8	1242	4	US-08-433-888-1	Sequence 1, Appl1
170	33	3.8	936	2	US-08-557-309B-21	Sequence 21, Appl1	243	33	3.8	1242	4	US-08-174-739-1	Sequence 1, Appl1
171	33	3.8	936	2	US-08-834-306-21	Sequence 21, Appl1	244	33	3.8	1242	4	US-08-434-256-1	Sequence 1, Appl1
172	33	3.8	936	4	US-08-993-674A-21	Sequence 21, Appl1	245	33	3.8	1265	4	US-08-991-789A-169	Sequence 169, Appl
173	33	3.8	936	4	US-09-256-976-21	Sequence 21, Appl1	246	33	3.8	1265	4	US-09-062-451-169	Sequence 169, Appl

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252	33	3.8	1273	4	US-09-599-661-1	Sequence 1, Appli	325	33	3.8	1737	2	US-08-805-478-3	Sequence 3, Appli
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274	33	3.8	1400	4	US-09-207-359B-40	Sequence 40, Appli	347	33	3.8	1868	4	US-09-676-610B-56	Sequence 1, Appli
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278	33	3.8	1461	4	US-08-723-126A-4	Sequence 4, Appli	351	33	3.8	1910	2	US-09-009-438-1	Sequence 1, Appli
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281	33	3.8	1474	4	US-08-821-994-64	Sequence 87, Appli	354	33	3.8	1964	3	US-08-468-856B-7	Sequence 7, Appli
282	33	3.8	1481	2	US-08-474-379C-87	Sequence 1, Appli	355	33	3.8	1968	4	US-08-468-856B-7	Sequence 68, Appli
283	33	3.8	1481	2	US-09-262-749-1	Sequence 39, Appli	356	33	3.8	1984	4	US-09-232-197-6	Sequence 68, Appli
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285	33	3.8	1490	2	US-08-553-367A-5	Sequence 5, Appli	358	33	3.8	1998	4	US-09-332-201-6	Sequence 26, Appli
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287	33	3.8	1490	4	US-09-734-719-5	Sequence 1, Appli	360	33	3.8	2000	4	US-09-605-785-374	Sequence 374, App
288	33	3.8	1502	2	US-08-651-940-1	Sequence 1, Appli	361	33	3.8	2000	4	US-09-439-313-374	Sequence 374, App
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292	33	3.8	1522	4	US-09-413-574-1	Sequence 311, App	365	33	3.8	2055	4	US-09-370-473-5	Sequence 3, Appli
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294	33	3.8	1540	3	US-08-977-001-2	Sequence 7, Appli	367	33	3.8	2087	4	US-09-332-197-6	Sequence 6, Appli
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302	33	3.8	1578	4	US-09-665-309-1	Sequence 1, Appli	375	33	3.8	2196	4	US-09-149-476-163	Sequence 163, App
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305	33	3.8	1582	3	US-08-545-196B-12	Sequence 12, Appli	378	33	3.8	2222	3	US-09-197-380-1	Sequence 24, Appli
306	33	3.8	1604	1	US-08-665-966-9	Sequence 9, Appli	379	33	3.8	2222	3	US-08-871-572B-3	Sequence 3, Appli
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310	33	3.8	1639	4	US-09-162-473-5	Sequence 5, Appli	383	33	3.8	2237	2	US-09-177-909-1	Sequence 1, Appli
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312	33	3.8	1646	4	US-09-062-451-290	Sequence 290, App	385	33	3.8	2255	4	US-08-871-572B-3	Sequence 3, Appli
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315	33	3.8	1659	1	US-08-463-694-7	Sequence 7, Appli	388	33	3.8	2301	4	US-09-232-197-8	Sequence 8, Appli
316	33	3.8	1659	1	US-08-694-501-7	Sequence 7, Appli	389	33	3.8	2301	4	US-09-232-197-8	Sequence 8, Appli
317	33	3.8	1659	1	US-08-548-509-4	Sequence 4, Appli	390	33	3.8	2301	4	US-09-232-197-8	Sequence 8, Appli
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319	33	3.8	1700	3	US-09-252-329-4	Sequence 4, Appli	392	33	3.8	2301	4	US-09-232-201-8	Sequence 8, Appli

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394	33	3	8	2320	4	US-09-978-197-1	Sequence 1, Appl	467	33	3	8	3417	4	US-08-860-339-17	Sequence 110, App
395	33	3	8	2338	4	US-09-232-200-66	Sequence 66, Appl	468	33	3	8	3527	2	US-08-909-965C-7	Sequence 7, Appl
396	33	3	8	2338	4	US-09-232-197-66	Sequence 66, Appl	469	33	3	8	3581	2	US-08-738-349-1	Sequence 1, Appl
397	33	3	8	2338	4	US-09-232-201-66	Sequence 66, Appl	470	33	3	8	3582	4	US-09-402-932-1	Sequence 1, Appl
398	33	3	8	2378	4	US-08-802-805D-20	Sequence 20, Appl	471	33	3	8	3680	4	US-09-647-390-15	Sequence 15, Appl
399	33	3	8	2399	4	US-09-385-801-1	Sequence 1, Appl	472	33	3	8	3709	4	US-09-541-782-7	Sequence 7, Appl
400	33	3	8	2405	1	US-08-454-097-30	Sequence 30, Appl	473	33	3	8	3709	4	US-09-723-820-7	Sequence 7, Appl
401	33	3	8	2405	1	US-08-185-359-30	Sequence 30, Appl	474	33	3	8	3825	4	US-09-208-742-3	Sequence 3, Appl
402	33	3	8	2409	4	US-09-293-322C-8	Sequence 8, Appl	475	33	3	8	4482	2	US-08-567-508C-1	Sequence 1, Appl
403	33	3	8	2424	4	US-09-149-476-228	Sequence 228, App	476	33	3	8	4482	2	US-09-196-480-1	Sequence 1, Appl
404	33	3	8	2484	4	US-09-293-325C-4	Sequence 4, Appl	477	33	3	8	4665	3	US-08-948-378A-7	Sequence 7, Appl
405	33	3	8	2502	4	US-09-234-332-1	Sequence 1, Appl	478	33	3	8	4665	3	US-09-164-425C-7	Sequence 7, Appl
406	33	3	8	2559	6	5258287-23	Patent No. 5258287	479	33	3	8	4931	4	US-08-726-320-2	Sequence 2, Appl
407	33	3	8	2589	4	US-08-569-749-1	Sequence 1, Appl	480	33	3	8	4931	4	US-09-208-716-2	Sequence 2, Appl
408	33	3	8	2589	4	PCT-US86-12860-1	Sequence 1, Appl	481	33	3	8	5803	2	US-08-726-012B-1	Sequence 1, Appl
409	33	3	8	2601	4	US-08-569-749-1	Sequence 1, Appl	482	33	3	8	6200	4	US-09-439-923-1	Sequence 1, Appl
410	33	3	8	2601	4	PCT-US86-12860-3	Sequence 3, Appl	483	33	3	8	6638	2	US-08-070-901-2	Sequence 2, Appl
411	33	3	8	2619	4	US-08-983-502-17	Sequence 17, Appl	484	33	3	8	58827	4	US-09-813-133A-3	Sequence 3, Appl
412	33	3	8	2619	5	PCT-US96-10521-17	Sequence 17, Appl	485	33	3	8	59665	4	US-09-813-817-3	Sequence 3, Appl
413	33	3	8	2625	4	US-09-645-041-18	Sequence 18, Appl	486	33	3	8	59665	4	US-09-978-197-3	Sequence 3, Appl
414	33	3	8	2628	2	US-08-696-944-1	Sequence 1, Appl	487	33	3	8	80246	4	US-09-478-294-4	Sequence 4, Appl
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416	33	3	8	2654	2	US-08-818-514-2	Sequence 2, Appl	489	33	3	7	36	4	US-09-078-294-4	Sequence 4, Appl
417	33	3	8	2654	3	US-09-115-934A-1	Sequence 1, Appl	490	33	3	7	37	4	US-08-113-646A-4	Sequence 44, Appl
418	33	3	8	2654	3	US-09-115-934A-2	Sequence 2, Appl	491	33	3	7	40	2	US-08-771-624B-1	Sequence 1, Appl
419	33	3	8	2658	2	US-08-592-383-3	Sequence 3, Appl	492	33	3	7	40	2	US-08-440-209-4	Sequence 4, Appl
420	33	3	8	2671	6	5168051-9	Patent No. 5168051	493	33	3	7	40	3	US-08-440-209-4	Sequence 4, Appl
421	33	3	8	2710	4	US-09-232-200-44	Sequence 44, Appl	494	33	3	7	40	4	US-09-732-067-7	Sequence 7, Appl
422	33	3	8	2710	4	US-09-232-200-70	Sequence 44, Appl	495	33	3	7	44	1	US-08-113-646A-40	Sequence 40, Appl
423	33	3	8	2710	4	US-09-232-197-44	Sequence 44, Appl	496	33	3	7	50	1	US-08-420-443-1	Sequence 1, Appl
424	33	3	8	2710	4	US-09-232-197-70	Sequence 44, Appl	497	33	3	7	52	4	US-09-415-784-23	Sequence 23, Appl
425	33	3	8	2710	4	US-09-232-201-44	Sequence 44, Appl	498	33	3	7	52	4	US-09-415-785A-23	Sequence 23, Appl
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432	33	3	8	2836	4	US-09-005-051-24	Sequence 24, Appl	505	33	3	7	58	2	US-08-231-565A-40	Sequence 40, Appl
433	33	3	8	2837	2	US-08-993-228-11	Sequence 11, Appl	506	33	3	7	58	2	US-09-007-961-40	Sequence 40, Appl
434	33	3	8	2837	4	US-08-983-502-14	Sequence 14, Appl	507	33	3	7	58	4	US-09-067-431-42	Sequence 42, Appl
435	33	3	8	2887	5	PCT-US96-10521-14	Sequence 14, Appl	508	33	3	7	60	1	US-08-241-465B-11	Sequence 11, Appl
436	33	3	8	2897	2	US-08-927-394-1	Sequence 1, Appl	509	33	3	7	60	1	US-08-241-465B-11	Sequence 11, Appl
437	33	3	8	2907	4	US-09-232-200-52	Sequence 52, Appl	510	33	3	7	61	4	US-09-457-959-8	Sequence 8, Appl
438	33	3	8	2907	4	US-09-232-197-52	Sequence 52, Appl	511	33	3	7	61	4	US-09-457-959-7	Sequence 7, Appl
439	33	3	8	2907	4	US-09-232-201-52	Sequence 52, Appl	512	33	3	7	65	4	US-09-415-784-32	Sequence 32, Appl
440	33	3	8	2917	4	US-09-232-200-26	Sequence 26, Appl	513	33	3	7	65	4	US-08-944-465-32	Sequence 32, Appl
441	33	3	8	2917	4	US-09-332-197-26	Sequence 26, Appl	514	33	3	7	65	4	US-09-415-868-32	Sequence 32, Appl
442	33	3	8	2917	4	US-09-332-201-26	Sequence 26, Appl	515	33	3	7	65	4	US-09-415-868-32	Sequence 32, Appl
443	33	3	8	2940	2	US-08-592-383-1	Sequence 1, Appl	516	33	3	7	65	1	US-08-702-344-7	Sequence 7, Appl
444	33	3	8	2940	6	5171671-1	Patent No. 5171671	517	33	3	7	69	1	US-08-702-344-7	Sequence 7, Appl
445	33	3	8	2992	4	US-09-334-601-11	Sequence 11, Appl	518	33	3	7	79	1	US-08-702-344-7	Sequence 7, Appl
446	33	3	8	3073	1	US-07-688-352C-31	Sequence 31, Appl	519	33	3	7	70	2	US-08-702-344-7	Sequence 7, Appl
447	33	3	8	3073	2	US-08-474-379C-31	Sequence 31, Appl	520	33	3	7	75	1	US-08-776-944-12	Sequence 12, Appl
448	33	3	8	3073	3	US-09-146-249A-31	Sequence 31, Appl	521	33	3	7	80	1	US-07-920-281C-25	Sequence 25, Appl
449	33	3	8	3073	3	US-08-206-188B-31	Sequence 31, Appl	522	33	3	7	80	4	US-08-466-277-25	Sequence 25, Appl
450	33	3	8	3073	5	PCT-US91-02714-30	Sequence 30, Appl	523	33	3	7	84	1	US-08-664-596B-3	Sequence 3, Appl
451	33	3	8	3131	1	US-07-688-352C-21	Sequence 21, Appl	524	33	3	7	84	1	US-08-738-367-3	Sequence 3, Appl
452	33	3	8	3131	1	US-09-146-249A-21	Sequence 21, Appl	525	33	3	7	85	1	US-08-120-827-97	Sequence 97, Appl
453	33	3	8	3131	1	US-08-206-188B-21	Sequence 21, Appl	526	33	3	7	85	1	US-08-120-827-97	Sequence 97, Appl
454	33	3	8	3131	5	PCT-US91-02714-20	Sequence 20, Appl	527	33	3	7	90	1	US-08-677-944-2	Sequence 1, Appl
455	33	3	8	3159	4	US-09-437-054A-7	Sequence 7, Appl	528	33	3	7	90	1	US-08-677-944-2	Sequence 1, Appl
456	33	3	8	3214	1	US-08-484-105-17	Sequence 17, Appl	529	33	3	7	90	4	US-09-065-058-16	Sequence 16, Appl
457	33	3	8	3214	1	US-08-484-105-17	Sequence 17, Appl	530	33	3	7	90	4	US-09-065-058-16	Sequence 16, Appl
458	33	3	8	3244	3	US-09-165-543-4	Sequence 4, Appl	531	33	3	7	90	4	US-09-921-203-1	Sequence 1, Appl
459	33	3	8	3375	4	US-09-511-625B-67	Sequence 67, Appl	532	33	3	7	91	4	US-09-404-879A-201	Sequence 201, App
460	33	3	8	3410	4	US-09-020-956-110	Sequence 110, App	533	33	3	7	94	4	US-09-404-879A-261	Sequence 261, App
461	33	3	8	3410	4	US-09-030-607-110	Sequence 110, App	534	33	3	7	98	1	US-08-088-658-42	Sequence 42, Appl
462	33	3	8	3410	4	US-09-605-785-110	Sequence 110, App	535	33	3	7	100	4	US-08-471-907A-42	Sequence 42, Appl
463	33	3	8	3410	4	US-09-439-313-110	Sequence 110, App	536	33	3	7	100	4	US-08-391-789A-30	Sequence 30, Appl
464	33	3	8	3410	4	US-09-352-616A-110	Sequence 110, App	537	33	3	7	100	4	US-09-062-451-30	Sequence 30, Appl
465	33	3	8	3410	4	US-09-602-877A-100	Sequence 100, App	538	33	3	7	101	4	US-09-598-326-30	Sequence 30, Appl
								539	33	3	7	101	4	US-09-404-879A-293	Sequence 293, App

539	32	3.7	105	2	US-08-735-381-2	Sequence 2, Appl1	C 612	32	3.7	470	4	US-09-439-313-102	Sequence 102, App
540	32	3.7	105	3	US-09-183-619-1	Sequence 1, Appl1	C 613	32	3.7	470	4	US-09-352-616A-102	Sequence 102, App
541	32	3.7	105	3	US-09-201-674-2	Sequence 2, Appl1	C 614	32	3.7	470	4	US-09-232-149A-102	Sequence 102, App
542	32	3.7	111	4	US-09-297-535-23	Sequence 23, Appl1	C 615	32	3.7	474	4	US-08-516-859A-97	Sequence 97, Appl1
543	32	3.7	117	1	US-08-702-344-3	Sequence 3, Appl1	C 616	32	3.7	474	4	US-09-586-472-97	Sequence 97, Appl1
544	32	3.7	121	4	US-09-297-535-20	Sequence 20, Appl1	C 617	32	3.7	474	4	US-09-528-706-97	Sequence 29, Appl1
545	32	3.7	130	6	5198345-15	Patent No. 5198345	C 618	32	3.7	502	4	US-08-186-276B-29	Sequence 29, Appl1
546	32	3.7	130	6	5198345-15	Patent No. 5198345	C 619	32	3.7	502	4	US-08-842-445-29	Sequence 29, Appl1
547	32	3.7	184	4	US-09-480-921B-13	Sequence 13, Appl1	C 620	32	3.7	502	4	US-09-186-188B-29	Sequence 29, Appl1
548	32	3.7	198	1	US-08-330-108-16	Sequence 16, Appl1	C 621	32	3.7	509	4	US-09-030-607-202	Sequence 202, App
549	32	3.7	198	5	PCT-US92-10087-16	Sequence 16, Appl1	C 622	32	3.7	509	4	US-09-030-607-202	Sequence 202, App
550	32	3.7	208	1	US-08-886-878A-37	Sequence 37, Appl1	C 623	32	3.7	509	4	US-09-605-785-202	Sequence 202, App
551	32	3.7	208	2	US-08-967-101-98	Sequence 98, Appl1	C 624	32	3.7	509	4	US-09-439-313-202	Sequence 202, App
552	32	3.7	208	2	US-08-592-541-98	Sequence 98, Appl1	C 625	32	3.7	509	4	US-09-352-616A-202	Sequence 202, App
553	32	3.7	208	2	US-09-124-698-98	Sequence 98, Appl1	C 626	32	3.7	515	3	US-08-589-028-1	Sequence 1, Appl1
554	32	3.7	208	4	US-09-127-480-98	Sequence 98, Appl1	C 627	32	3.7	515	3	US-08-784-582-1	Sequence 1, Appl1
555	32	3.7	208	4	US-08-496-841C-98	Sequence 98, Appl1	C 628	32	3.7	515	3	US-08-785-271-1	Sequence 12, Appl1
556	32	3.7	208	4	US-09-175-928-37	Sequence 37, Appl1	C 629	32	3.7	528	1	US-08-341-568-1	Sequence 1, Appl1
557	32	3.7	208	4	US-09-124-523-98	Sequence 98, Appl1	C 630	32	3.7	536	2	US-08-911-020-1	Sequence 1, Appl1
558	32	3.7	227	4	US-08-520-678A-28	Sequence 28, Appl1	C 631	32	3.7	536	2	US-08-911-020-1	Sequence 1, Appl1
559	32	3.7	227	4	US-08-897-126-28	Sequence 28, Appl1	C 632	32	3.7	556	4	US-09-370-838-242	Sequence 242, App
560	32	3.7	227	4	US-09-191-136-29	Sequence 29, Appl1	C 633	32	3.7	572	4	US-09-328-111-644	Sequence 644, App
561	32	3.7	253	2	US-08-520-678A-25	Sequence 25, Appl1	C 634	32	3.7	572	4	US-09-342-653-5	Sequence 5, Appl1
562	32	3.7	253	4	US-08-897-126-25	Sequence 25, Appl1	C 635	32	3.7	578	4	US-09-385-982-203	Sequence 757, App
563	32	3.7	257	4	US-08-520-678A-24	Sequence 24, Appl1	C 636	32	3.7	578	4	US-09-602-877A-95	Sequence 95, Appl1
564	32	3.7	257	4	US-08-897-126-24	Sequence 24, Appl1	C 637	32	3.7	581	2	US-08-557-309B-22	Sequence 22, Appl1
565	32	3.7	260	4	US-08-520-678A-29	Sequence 29, Appl1	C 638	32	3.7	581	4	US-08-834-306-22	Sequence 22, Appl1
566	32	3.7	260	4	US-08-897-126-26	Sequence 26, Appl1	C 639	32	3.7	581	4	US-08-993-674A-22	Sequence 22, Appl1
567	32	3.7	263	4	US-09-031-097-26	Sequence 26, Appl1	C 640	32	3.7	581	4	US-09-256-976-22	Sequence 22, Appl1
568	32	3.7	270	2	US-08-520-678A-30	Sequence 30, Appl1	C 641	32	3.7	588	4	US-09-385-982-128	Sequence 128, App
569	32	3.7	270	2	US-08-897-126-30	Sequence 30, Appl1	C 642	32	3.7	588	4	US-08-150-331-45	Sequence 45, Appl1
570	32	3.7	271	2	US-08-731-272A-29	Sequence 29, Appl1	C 643	32	3.7	596	1	US-08-150-331-45	Sequence 147, App
571	32	3.7	288	2	US-08-648-496-1	Sequence 1, Appl1	C 644	32	3.7	599	4	US-09-328-111-147	Sequence 6, Appl1
572	32	3.7	290	4	US-09-232-575-20	Sequence 20, Appl1	C 645	32	3.7	603	2	US-08-924-838-6	Sequence 376, App
573	32	3.7	291	4	US-09-329-796-13	Sequence 13, Appl1	C 646	32	3.7	603	4	US-09-385-982-293	Sequence 293, App
574	32	3.7	296	2	US-09-032-684-13	Sequence 13, Appl1	C 647	32	3.7	611	4	US-09-105-542A-2	Sequence 2, Appl1
575	32	3.7	298	2	US-08-520-678A-21	Sequence 21, Appl1	C 648	32	3.7	615	4	US-09-105-542A-2	Sequence 2, Appl1
576	32	3.7	298	4	US-08-897-126-21	Sequence 21, Appl1	C 649	32	3.7	624	4	US-09-385-982-376	Sequence 376, App
577	32	3.7	308	2	US-08-721-488-4	Sequence 4, Appl1	C 650	32	3.7	624	4	US-09-385-982-305	Sequence 305, App
578	32	3.7	314	1	US-08-686-878A-25	Sequence 25, Appl1	C 651	32	3.7	630	1	US-08-185-414E-1	Sequence 1, Appl1
579	32	3.7	314	4	US-09-175-928-25	Sequence 25, Appl1	C 652	32	3.7	635	1	US-08-416-336-5	Sequence 35, Appl1
580	32	3.7	321	4	US-08-520-678A-23	Sequence 23, Appl1	C 653	32	3.7	635	2	US-08-416-336-5	Sequence 35, Appl1
581	32	3.7	321	4	US-08-897-126-23	Sequence 23, Appl1	C 654	32	3.7	635	2	US-08-456-460C-35	Sequence 35, Appl1
582	32	3.7	326	4	US-09-629-645A-17	Sequence 17, Appl1	C 655	32	3.7	635	5	PCT-US94A-05314-15	Sequence 35, Appl1
583	32	3.7	327	4	US-09-385-982-544	Sequence 544, App	C 656	32	3.7	635	5	US-09-385-982-327	Sequence 327, App
584	32	3.7	334	2	US-09-032-684-8	Sequence 8, Appl1	C 657	32	3.7	684	1	US-08-226-264-27	Sequence 27, Appl1
585	32	3.7	337	2	US-09-032-684-11	Sequence 11, Appl1	C 658	32	3.7	685	4	US-09-227-357-66	Sequence 66, Appl1
586	32	3.7	337	2	US-08-520-678A-22	Sequence 22, Appl1	C 659	32	3.7	688	6	5498694-3	Patent No. 5498694
587	32	3.7	356	2	US-08-897-126-22	Sequence 22, Appl1	C 660	32	3.7	692	4	US-09-328-111-285	Sequence 285, App
588	32	3.7	374	2	US-08-370-156-24	Sequence 24, Appl1	C 661	32	3.7	700	1	US-07-846-992-1	Sequence 1, Appl1
589	32	3.7	374	4	US-09-385-982-494	Sequence 494, App	C 662	32	3.7	700	1	US-08-469-555-1	Sequence 26, Appl1
590	32	3.7	380	1	US-08-126-587C-5	Sequence 5, Appl1	C 663	32	3.7	703	4	US-09-152-060-26	Sequence 6, Appl1
591	32	3.7	393	4	US-09-605-785-357	Sequence 357, App	C 664	32	3.7	703	4	US-09-313-300-6	Sequence 318, App
592	32	3.7	393	4	US-09-493-313-357	Sequence 357, App	C 665	32	3.7	712	4	US-09-149-476-318	Sequence 15, Appl1
593	32	3.7	393	4	US-09-352-616A-357	Sequence 21, Appl1	C 666	32	3.7	712	4	US-09-437-054A-15	Sequence 66, Appl1
594	32	3.7	395	4	US-09-195-106-21	Sequence 21, Appl1	C 667	32	3.7	732	4	US-07-847-010-12	Sequence 12, Appl1
595	32	3.7	403	4	US-09-387-212-2	Sequence 2, Appl1	C 668	32	3.7	732	4	US-08-530-165-1	Sequence 1, Appl1
596	32	3.7	403	4	US-09-948-802-2	Sequence 2, Appl1	C 669	32	3.7	756	2	US-08-938-675A-1	Sequence 20, Appl1
597	32	3.7	413	4	US-09-227-357-71	Sequence 71, Appl1	C 670	32	3.7	770	3	US-09-149-476-20	Sequence 6, Appl1
598	32	3.7	429	1	US-08-686-878A-8	Sequence 8, Appl1	C 671	32	3.7	773	4	US-09-361-434-8	Sequence 8, Appl1
599	32	3.7	429	1	US-09-175-928-13	Sequence 13, Appl1	C 672	32	3.7	775	3	US-09-361-434-8	Sequence 8, Appl1
600	32	3.7	433	1	US-07-987-272A-13	Sequence 13, Appl1	C 673	32	3.7	775	4	US-09-635-025-6	Sequence 6, Appl1
601	32	3.7	450	2	US-08-592-541-7	Sequence 7, Appl1	C 674	32	3.7	780	2	US-09-635-025-6	Sequence 6, Appl1
602	32	3.7	450	2	US-08-967-101-7	Sequence 7, Appl1	C 675	32	3.7	780	2	US-08-440-804-36	Sequence 36, Appl1
603	32	3.7	450	2	US-09-124-698-7	Sequence 7, Appl1	C 676	32	3.7	789	4	US-08-590-399-36	Sequence 36, Appl1
604	32	3.7	450	4	US-09-127-480-7	Sequence 7, Appl1	C 677	32	3.7	789	4	US-09-020-956-32	Sequence 32, Appl1
605	32	3.7	450	4	US-08-496-841C-7	Sequence 7, Appl1	C 678	32	3.7	789	4	US-09-030-607-32	Sequence 32, Appl1
606	32	3.7	450	4	US-09-124-523-7	Sequence 7, Appl1	C 679	32	3.7	789	4	US-09-605-785-32	Sequence 32, Appl1
607	32	3.7	464	4	US-09-302-769-37	Sequence 37, Appl1	C 680	32	3.7	789	4	US-09-439-313-32	Sequence 32, Appl1
608	32	3.7	467	2	US-08-841-349-18	Sequence 18, Appl1	C 681	32	3.7	789	4	US-09-352-616A-32	Sequence 32, Appl1
609	32	3.7	470	4	US-09-020-956-102	Sequence 102, App	C 682	32	3.7	789	4	US-09-232-149A-32	Sequence 32, Appl1
610	32	3.7	470	4	US-09-030-607-102	Sequence 102, App	C 683	32	3.7	790	4	US-09-461-474-13	Sequence 13, Appl1
611	32	3.7	470	4	US-09-605-785-102	Sequence 102, App	C 684	32	3.7	790	4	US-09-461-474-13	Sequence 13, Appl1

685	32	3.7	794	4	US-09-385-982-537	Sequence 537, App	758	32	3.7	1013	1	US-08-314-586-30	Sequence 30, Appl
686	32	3.7	804	4	US-09-149-476-125	Sequence 125, App	759	32	3.7	1023	1	US-08-252-966B-16	Sequence 16, Appl
687	32	3.7	806	4	US-08-955-629C-1	Sequence 1, Appl	760	32	3.7	1027	4	US-09-344-529-1	Sequence 1, Appl
688	32	3.7	809	4	US-09-149-476-244	Sequence 244, App	761	32	3.7	1027	4	US-09-465-558-57	Sequence 57, Appl
689	32	3.7	817	4	US-08-885-469-1	Sequence 1, Appl	762	32	3.7	1032	4	US-09-257-179-21	Sequence 21, Appl
690	32	3.7	817	4	US-09-625-918-1	Sequence 1, Appl	763	32	3.7	1033	4	US-09-173-300-46	Sequence 46, Appl
691	32	3.7	826	4	US-08-658-551-3	Sequence 3, Appl	764	32	3.7	1037	4	US-09-257-179-16	Sequence 16, Appl
692	32	3.7	826	4	US-08-602-228-3	Sequence 3, Appl	765	32	3.7	1046	1	US-08-361-467B-4	Sequence 4, Appl
693	32	3.7	826	4	US-08-649-341A-3	Sequence 3, Appl	766	32	3.7	1046	1	US-08-484-332C-4	Sequence 4, Appl
694	32	3.7	826	4	US-08-440-440B-3	Sequence 3, Appl	767	32	3.7	1047	1	US-08-403-378B-3	Sequence 3, Appl
695	32	3.7	826	4	US-08-533-901B-3	Sequence 3, Appl	768	32	3.7	1051	4	US-09-245-041-10	Sequence 10, Appl
696	32	3.7	826	4	US-08-839-031A-3	Sequence 3, Appl	769	32	3.7	1052	4	US-09-592-891A-8	Sequence 8, Appl
697	32	3.7	826	4	US-08-839-031A-3	Sequence 3, Appl	770	32	3.7	1056	4	US-08-157-101A-4	Sequence 4, Appl
698	32	3.7	826	4	US-09-185-258C-3	Sequence 3, Appl	771	32	3.7	1078	4	US-09-452-239-41	Sequence 41, Appl
699	32	3.7	826	4	PCT-US95-12724-3	Sequence 3, Appl	772	32	3.7	1080	4	US-08-425-757B-1	Sequence 1, Appl
700	32	3.7	836	5	US-08-658-805-7	Sequence 7, Appl	773	32	3.7	1080	2	US-08-722-050-1	Sequence 1, Appl
701	32	3.7	857	1	US-08-308-883-1	Sequence 1, Appl	774	32	3.7	1092	4	US-09-227-357-35	Sequence 35, Appl
702	32	3.7	857	1	US-08-730-163-1	Sequence 1, Appl	775	32	3.7	1098	3	US-09-248-335-35	Sequence 35, Appl
703	32	3.7	857	4	US-08-256-799-1	Sequence 1, Appl	776	32	3.7	1106	3	US-09-361-434-16	Sequence 16, Appl
704	32	3.7	857	4	US-08-462-437-1	Sequence 1, Appl	777	32	3.7	1106	3	US-09-361-434-16	Sequence 16, Appl
705	32	3.7	859	4	US-09-247-373B-47	Sequence 47, Appl	778	32	3.7	1106	4	US-09-635-025-16	Sequence 16, Appl
706	32	3.7	860	1	US-07-847-010-18	Sequence 18, Appl	779	32	3.7	1106	4	US-09-635-025-16	Sequence 16, Appl
707	32	3.7	872	4	US-09-248-335-63	Sequence 63, Appl	780	32	3.7	1116	3	US-08-916-443A-16	Sequence 16, Appl
708	32	3.7	873	4	US-09-475-362A-20	Sequence 20, Appl	781	32	3.7	1128	3	US-09-372-422A-23	Sequence 23, Appl
709	32	3.7	879	1	US-08-158-682A-1	Sequence 1, Appl	782	32	3.7	1128	3	US-09-372-422A-23	Sequence 23, Appl
710	32	3.7	879	1	US-08-015-203-1	Sequence 1, Appl	783	32	3.7	1129	4	US-09-227-357-40	Sequence 40, Appl
711	32	3.7	880	1	US-08-616-368A-7	Sequence 7, Appl	784	32	3.7	1134	3	US-09-248-335-29	Sequence 29, Appl
712	32	3.7	880	4	US-09-054-298-7	Sequence 7, Appl	785	32	3.7	1146	4	US-09-452-239-3	Sequence 3, Appl
713	32	3.7	880	4	US-09-247-373B-39	Sequence 39, Appl	786	32	3.7	1147	1	US-08-665-716-1-1	Sequence 1, Appl
714	32	3.7	880	4	US-08-818-655-7	Sequence 7, Appl	787	32	3.7	1149	4	US-09-227-357-84	Sequence 84, Appl
715	32	3.7	882	2	US-08-909-965C-9	Sequence 9, Appl	788	32	3.7	1153	4	US-09-149-476-41	Sequence 41, Appl
716	32	3.7	888	1	US-08-173-510B-99	Sequence 99, Appl	789	32	3.7	1159	4	US-09-100-391-5	Sequence 5, Appl
717	32	3.7	888	1	US-08-458-218-97	Sequence 97, Appl	790	32	3.7	1161	4	US-09-149-476-310	Sequence 310, Appl
718	32	3.7	888	2	US-08-450-497-99	Sequence 99, Appl	791	32	3.7	1182	4	US-09-469-242-1	Sequence 1, Appl
719	32	3.7	888	3	US-09-188-930-13	Sequence 13, Appl	792	32	3.7	1183	4	US-09-372-422A-23	Sequence 23, Appl
720	32	3.7	893	1	US-08-276-452A-66	Sequence 66, Appl	793	32	3.7	1206	4	US-09-465-558-53	Sequence 53, Appl
721	32	3.7	893	2	US-08-798-744-66	Sequence 66, Appl	794	32	3.7	1210	4	US-09-443-074A-29	Sequence 29, Appl
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723	32	3.7	911	4	US-09-227-357-109	Sequence 109, Appl	796	32	3.7	1214	4	US-09-605-785-225	Sequence 225, Appl
724	32	3.7	911	4	US-09-364-230-25	Sequence 25, Appl	797	32	3.7	1214	4	US-09-439-313-225	Sequence 225, Appl
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726	32	3.7	913	4	US-09-229-911A-13	Sequence 13, Appl	799	32	3.7	1215	4	US-09-232-149A-225	Sequence 225, Appl
727	32	3.7	917	4	US-09-227-357-43	Sequence 43, Appl	800	32	3.7	1215	1	US-08-592-214A-1	Sequence 1, Appl
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729	32	3.7	919	3	US-09-248-335-19	Sequence 19, Appl	802	32	3.7	1215	3	US-09-149-976-1	Sequence 1, Appl
730	32	3.7	921	4	US-09-227-357-30	Sequence 30, Appl	803	32	3.7	1215	4	US-09-605-785-326	Sequence 326, Appl
731	32	3.7	940	2	US-08-471-717-1	Sequence 1, Appl	804	32	3.7	1215	4	US-09-439-313-326	Sequence 326, Appl
732	32	3.7	940	4	US-09-069-023-9	Sequence 9, Appl	805	32	3.7	1215	4	US-09-352-616A-336	Sequence 336, Appl
733	32	3.7	940	4	US-09-069-023-9	Sequence 9, Appl	806	32	3.7	1215	4	US-09-352-616A-336	Sequence 336, Appl
734	32	3.7	943	4	US-09-149-476-35	Sequence 35, Appl	807	32	3.7	1215	6	5169941-7	Patent No. 5169941
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737	32	3.7	953	2	US-08-636-176-1	Sequence 1, Appl	810	32	3.7	1217	4	US-08-286-020-1	Sequence 1, Appl
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749	32	3.7	991	4	US-09-344-529-3	Sequence 3, Appl	822	32	3.7	1279	3	US-09-248-335-25	Sequence 25, Appl
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and is derived by analysis of the total score distribution.

SUMMARIES

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49	39	4.5	355	9	AL729765
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51	39	4.5	370	10	AM694961
52	39	4.5	403	10	AW394575
53	39	4.5	408	9	AI395258
54	39	4.5	408	9	AI395258
55	39	4.5	410	12	BF344662
56	39	4.5	429	10	BE015394
57	39	4.5	445	12	BF499456
58	39	4.5	456	9	AI413964
59	39	4.5	489	9	AI093531
60	39	4.5	498	10	AV386050
61	39	4.5	500	13	BI342776
62	39	4.5	507	9	AL634744
63	39	4.5	509	12	BF534593
64	39	4.5	552	13	BM269012
65	39	4.5	555	14	BM942892
66	39	4.5	576	10	AM129897
67	39	4.5	586	9	AU033600
68	39	4.5	586	9	AI462326
69	39	4.5	608	14	BQ521126
70	39	4.5	801	17	CNS0385X
71	39	4.5	819	17	CNS028DXL
72	39	4.5	832	17	CNS00818
73	39	4.5	887	13	BI521705
74	39	4.5	948	13	BI489262
75	39	4.5	963	14	BQ440993
76	39	4.5	1069	12	BF129342
77	39	4.5	1079	13	BI489064
78	39	4.5			
79	39	4.5			

80	39	4.5	1101	17	CNS00CPC	AL059482 Drosophila	153	37	4.3	140	12	BG454124	BG454124 NP096G06L
81	39	4.5	1105	12	BE965491	BE965491 601659420	154	37	4.3	144	9	AT262151	AT262151 qz28e03.x
82	39	4.5	1405	13	BI489285	BI489285 603021628	155	37	4.3	144	9	AT734004	AT734004 qz28e03.x
83	39	4.5	1418	12	BG030516	BG030516 602288054	156	37	4.3	146	9	AT734004	AT734004 qz28e03.x
84	38	4.4	62	9	AA398875	AA398875 vdt1d04.x	157	37	4.3	148	12	BF750886	BF750886 RCI-BN042
85	38	4.4	100	13	BI001553	BI001553 MR3-HN014	158	37	4.3	152	14	BQ393689	BQ393689 NISC-NQ04
86	38	4.4	134	17	CNS03RFP	AL241378 Tetraodon	159	37	4.3	156	14	C25761	C25761 C25761 Dict
87	38	4.4	140	13	BG977694	BG977694 MR2-CI018	160	37	4.3	166	9	AT152279	AT152279 tx06e01.x
88	38	4.4	150	10	BE069307	BE069307 OV3-BT008	161	37	4.3	169	9	AT249689	AT249689 qz50h08.x
89	38	4.4	158	10	BE248148	BE248148 NF002A07D	162	37	4.3	174	10	BH588786	BH588786 BE588786
90	38	4.4	180	13	BJ332629	BJ332629 BJ332629	163	37	4.3	176	9	AT699784	AT699784 C212F04.x
91	38	4.4	236	10	AM432525	AM432525 bh75d08.y	164	37	4.3	189	13	BM270126	BM270126 sak24910.
92	38	4.4	240	9	AU074936	AU074936 AU074936	165	37	4.3	191	12	BE804703	BE804703 sr86a06.y
93	38	4.4	242	13	BI502406	BI502406 Kt49c10.y	166	37	4.3	194	10	AM306966	AM306966 sf51a10.y
94	38	4.4	248	13	BI704970	BI704970 Kt60909.y	167	37	4.3	192	12	BG237216	BG237216 saag8c08.
95	38	4.4	251	12	BF807864	BF807864 RC3-CI004	168	37	4.3	197	9	AT631876	AT631876 wa37b12.x
96	38	4.4	272	9	AL677222	AL677222 AL677222	169	37	4.3	207	9	AT323848	AT323848 mt66f09.x
97	38	4.4	275	13	BM346103	BM346103 Kt12d02.y	170	37	4.3	208	13	BM092633	BM092633 sash1566.
98	38	4.4	275	13	BQ455797	BQ455797 Kt22h12.y	171	37	4.3	209	13	BM092633	BM092633 sash1566.
99	38	4.4	278	14	BQ612645	BQ612645 sap72h02.	172	37	4.3	215	13	BG911154	BG911154 Kt76d08.y
100	38	4.4	300	9	AU263329	AU263329 AU263329	173	37	4.3	218	10	BE624780	BE624780 uu26c10.y
101	38	4.4	303	13	BG939743	BG939743 Cr61e04.x	174	37	4.3	219	9	AT1919434	AT1919434 cm84a05.x
102	38	4.4	317	13	BM280884	BM280884 K106d06.y	175	37	4.3	221	12	BG001296	BG001296 I10-GN028
103	38	4.4	326	10	AM785659	AM785659 117007.MA	176	37	4.3	222	12	BG651671	BG651671 sad59e08.
104	38	4.4	333	9	AU261286	AU261286 AU261286	177	37	4.3	228	12	CG2990	CG2990 C92990 Dict
105	38	4.4	339	14	BQ748672	BQ748672 UI-M-FA0-	178	37	4.3	237	9	AA576046	AA576046 tm88D08.s
106	38	4.4	352	9	AA021890	AA021890 NM82d12.x	179	37	4.3	240	9	AT824522	AT824522 Cx17d03.x
107	38	4.4	358	12	BG450094	BG450094 NF011C09D	180	37	4.3	240	12	BG841917	BG841917 MEST33-H0
108	38	4.4	368	14	W34411	W34411 ma98a08.r1	181	37	4.3	244	10	AM666166	AM666166 sK33a06.y
109	38	4.4	370	9	AL803313	AL803313 AL803313	182	37	4.3	254	9	AU094219	AU094219 AU094219
110	38	4.4	378	10	AM990222	AM990222 Uf35f02.y	183	37	4.3	254	9	AU094219	AU094219 AU094219
111	38	4.4	380	11	BC027649	BC027649 Mus muscu	184	37	4.3	259	13	BI001794	BI001794 MR3-HN015
112	38	4.4	386	14	C94469	C94469 C94469 Dict	185	37	4.3	260	14	BQ423248	BQ423248 B24a402.y
113	38	4.4	399	14	BG965590	BG965590 602830619	186	37	4.3	260	14	BQ423248	BQ423248 B24a402.y
114	38	4.4	429	14	BQ748073	BQ748073 UI-M-FA0-	187	37	4.3	270	9	AL635155	AL635155 AL635155
115	38	4.4	441	10	AM635529	AM635529 b140c02.w	188	37	4.3	274	12	BF634988	BF634988 NF077E08D
116	38	4.4	445	10	AM635591	AM635591 b141c02.w	189	37	4.3	276	10	AM423760	AM423760 sh51d07.y
117	38	4.4	455	13	BG926291	BG926291 HNC33-1-D	190	37	4.3	277	10	AM156888	AM156888 sab9b07.x
118	38	4.4	466	9	AL803394	AL803394 AL803394	191	37	4.3	281	13	BM521098	BM521098 sal34e07.
119	38	4.4	471	13	BI455249	BI455249 bh45e12.y	192	37	4.3	282	13	BI495456	BI495456 df118c08.
120	38	4.4	500	10	BE693203	BE693203 zewp0107	193	37	4.3	288	13	AM099060	AM099060 sd33g01.y
121	38	4.4	516	12	BE893404	BE893404 601436735	194	37	4.3	292	10	AM099060	AM099060 sd33g01.y
122	38	4.4	524	12	BG202913	BG202913 RST2281	195	37	4.3	292	10	AM099060	AM099060 sd33g01.y
123	38	4.4	555	10	BE408765	BE408765 601303457	196	37	4.3	294	13	BI742580	BI742580 Kc59d12.y
124	38	4.4	576	12	BE965901	BE965901 601659080	197	37	4.3	296	9	BI222889	BI222889 Kc09b11.y
125	38	4.4	578	14	BQ523351	BQ523351 NISC-1121	198	37	4.3	297	9	AT189894	AT189894 Kc38d12.x
126	38	4.4	616	2	BM830863	BM830863 K-EST0104	199	37	4.3	297	9	AT189894	AT189894 Kc38d12.x
127	38	4.4	628	9	AL667177	AL667177 AL667177	200	37	4.3	298	10	AM156318	AM156318 se22e06.y
128	38	4.4	638	17	AQ229622	AQ229622 MDX0044N	201	37	4.3	302	12	BG237811	BG237811 sab08e06.
129	38	4.4	675	10	BE573505	BE573505 601332513	202	37	4.3	308	14	BQ621347	BQ621347 3524.1.48
130	38	4.4	755	13	BI489221	BI489221 603021446	203	37	4.3	315	12	BF584526	BF584526 602098725
131	38	4.4	758	10	BE254113	BE254113 601113971	204	37	4.3	317	14	C90426	C90426 C90426
132	38	4.4	764	10	AM332484	AM332484 S9A9 AGS-	205	37	4.3	322	9	AT253089	AT253089 q375g09.x
133	38	4.4	766	11	BC018268	BC018268 Mus muscu	206	37	4.3	322	9	AT253089	AT253089 q375g09.x
134	38	4.4	832	12	BE729660	BE729660 601562804	207	37	4.3	322	9	AT253089	AT253089 q375g09.x
135	38	4.4	853	17	AZ545711	AZ545711 ENTGD19TF	208	37	4.3	322	9	AT253089	AT253089 q375g09.x
136	38	4.4	887	12	BF274559	BF274559 GA-ED002	209	37	4.3	322	9	AT253089	AT253089 q375g09.x
137	38	4.4	925	13	BM416279	BM416279 OP21369.M	210	37	4.3	322	9	AT253089	AT253089 q375g09.x
138	38	4.4	960	17	AG031602	AG031602 Pan trogl	211	37	4.3	322	9	AT253089	AT253089 q375g09.x
139	38	4.4	985	13	BM415996	BM415996 OP21079.M	212	37	4.3	322	9	AT253089	AT253089 q375g09.x
140	38	4.4	1000	13	BI521761	BI521761 603081730	213	37	4.3	322	9	AT253089	AT253089 q375g09.x
141	38	4.4	1012	14	BQ433017	BQ433017 AGENCOURT	214	37	4.3	322	9	AT253089	AT253089 q375g09.x
142	38	4.4	1090	14	BO717503	BO717503 AGENCOURT	215	37	4.3	322	9	AT253089	AT253089 q375g09.x
143	38	4.4	1101	17	CNS01406	AL104616 Drosophila	216	37	4.3	322	9	AT253089	AT253089 q375g09.x
144	38	4.4	1161	12	BG479771	BG479771 602526978	217	37	4.3	322	9	AT253089	AT253089 q375g09.x
145	38	4.4	1363	12	BE965813	BE965813 601655584	218	37	4.3	322	9	AT253089	AT253089 q375g09.x
146	38	4.4	1750	13	BG911020	BG911020 602806383	219	37	4.3	322	9	AT253089	AT253089 q375g09.x
147	38	4.4	72	14	T25592	T25592 EST00628.Un	220	37	4.3	322	9	AT253089	AT253089 q375g09.x
148	37	4.3	93	13	BG963829	BG963829 602831491	221	37	4.3	322	9	AT253089	AT253089 q375g09.x
149	37	4.3	111	14	BM966736	BM966736 K011b07.y	222	37	4.3	322	9	AT253089	AT253089 q375g09.x
150	37	4.3	124	9	AA616273	AA616273 vnt6a07.x	223	37	4.3	322	9	AT253089	AT253089 q375g09.x
151	37	4.3	126	13	BM541971	BM541971 AGENCOURT	224	37	4.3	322	9	AT253089	AT253089 q375g09.x
152	37	4.3	137	12	BF644938	BF644938 NF028A09E	225	37	4.3	322	9	AT253089	AT253089 q375g09.x

C 226	37	4.3	411	9	AI537079	AI537079 to82h04.x	C 229	36	4.2	106	9	AA49906	AA49906 aa52b09.s
227	37	4.3	411	13	BM521226	BM521226 sa112b08.	C 300	36	4.2	111	14	BQ225032	BQ225032 ACENCOURT
228	37	4.3	415	10	AV657079	AV657079	C 301	36	4.2	112	13	BG956245	BG956245 OV1-CT075
C 229	37	4.3	416	9	AL803452	AL803452	C 302	36	4.2	120	13	BM478091	BM478091 ACENCOURT
230	37	4.3	424	9	AU262968	AU262968	C 303	36	4.2	121	12	BF915483	BF915483 MR3-UT012
231	37	4.3	428	12	BE881033	BE881033 601490790	C 304	36	4.2	123	13	BI742035	BI742035 Kc89p07.y
232	37	4.3	440	13	BI936227	BI936227 PFE8TOa2	C 305	36	4.2	125	9	AU071541	AU071541 AU071541
C 233	37	4.3	464	9	AA659923	AA659923 nv03608.s	C 306	36	4.2	128	9	AU073398	AU073398 AU073398
C 234	37	4.3	464	9	AI138585	AI138585 CQ93f08.x	C 307	36	4.2	131	13	BQ237436	BQ237436 TE05016G
C 235	37	4.3	464	9	AU262244	AU262244	C 308	36	4.2	133	13	BI536278	BI536278 390802 MA
236	37	4.3	472	14	C93369	C93369 C93369 D1ct	C 309	36	4.2	135	12	BF381832	BF381832 602037926
C 237	37	4.3	477	10	AL636291	AL636291	C 310	36	4.2	137	13	BG950524	BG950524 PM0-CT070
C 238	37	4.3	484	10	AM584191	AM584191 N210131g	C 311	36	4.2	141	13	BU427681	BU427681 BU427681
C 239	37	4.3	486	10	AM544452	AM544452 C0181H12-	C 312	36	4.2	142	13	BU337720	BU337720 BU337720
C 240	37	4.3	492	10	AM641185	AM641185 cm04C09.w	C 313	36	4.2	143	13	BU3371067	BU3371067 BU3371067
C 241	37	4.3	494	9	AL641624	AL641624	C 314	36	4.2	144	9	AI944844	AI944844 bs06b03.y
C 242	37	4.3	494	9	BO395433	BO395433 NISC ng15	C 315	36	4.2	144	13	BI395033	BI395033 BI395033
C 243	37	4.3	518	14	BO527377	BO527377 NISC ng02	C 316	36	4.2	144	13	BI397854	BI397854 BI397854
C 244	37	4.3	524	12	BF015608	BF015608 uy23g02.y	C 317	36	4.2	145	10	AM169379	AM169379 KJ25f06.x
C 245	37	4.3	530	9	AI581183	AI581183 cl194f03.x	C 318	36	4.2	145	10	AM169379	AM169379 KJ25f06.x
C 246	37	4.3	533	9	AI691234	AI691234 606025H09	C 319	36	4.2	146	13	BI053612	BI053612 MR3-GN046
C 247	37	4.3	547	9	AU261551	AU261551	C 320	36	4.2	147	9	AI340603	AI340603 cb31g08.x
C 248	37	4.3	552	9	AI1395074	AI1395074 MA002345.	C 321	36	4.2	147	9	AI960330	AI960330 sc82a06.y
C 249	37	4.3	566	14	BO526714	BO526714 NISC no18	C 322	36	4.2	149	12	BE976721	BE976721 bs55a08.y
C 250	37	4.3	568	14	BO396965	BO396965 NISC ng25	C 323	36	4.2	150	9	AI267162	AI267162 aq49f03.x
C 251	37	4.3	570	14	BO522054	BO522054 NISC n114	C 324	36	4.2	150	9	AI965757	AI965757 sc75f09.y
C 252	37	4.3	577	14	BO395988	BO395988 NISC ng18	C 325	36	4.2	150	13	BU420264	BU420264 BU420264
C 253	37	4.3	582	14	BO393588	BO393588 NISC ng04	C 326	36	4.2	151	9	AI432935	AI432935 ch44d08.x
C 254	37	4.3	582	14	BO523951	BO523951 NISC no01	C 327	36	4.2	151	10	AM008265	AM008265 wv52e07.x
C 255	37	4.3	590	14	BO524387	BO524387 NISC no04	C 328	36	4.2	151	13	BI337913	BI337913 BI337913
C 256	37	4.3	592	10	BE038678	BE038678 AB04A02 A	C 329	36	4.2	152	13	BI521790	BI521790 BI521790
C 257	37	4.3	600	14	BO396574	BO396574 NISC ng21	C 330	36	4.2	152	13	BI364859	BI364859 BI364859
C 258	37	4.3	607	14	BO415149	BO415149 GA Ed009	C 331	36	4.2	152	13	BI366714	BI366714 BI366714
C 259	37	4.3	622	10	AM130525	AM130525 xff52e06.x	C 332	36	4.2	152	13	BI397535	BI397535 BI397535
C 260	37	4.3	623	13	BM013585	BM013585 603639061	C 333	36	4.2	153	9	AI037454	AI037454 DKF2P564A
C 261	37	4.3	629	14	BO398985	BO398985 NISC mg09	C 334	36	4.2	153	9	AI138406	AI138406 DKF2P762K
C 262	37	4.3	629	14	BO527405	BO527405 NISC no22	C 335	36	4.2	153	13	BI943053	BI943053 sn09D06.y
263	37	4.3	638	13	BI524025	BI524025 603052190	C 336	36	4.2	153	13	BI368665	BI368665 BI368665
264	37	4.3	642	13	BI822759	BI822759 603040213	C 337	36	4.2	153	13	BI393754	BI393754 BI393754
265	37	4.3	644	10	AM561968	AM561968 T8236 MVA	C 338	36	4.2	153	13	BI418243	BI418243 BI418243
C 267	37	4.3	668	10	AM766225	AM766225 da83h05.y	C 339	36	4.2	154	13	BI768472	BI768472 kJ20005.y
C 268	37	4.3	669	10	AV706671	AV706671	C 340	36	4.2	154	13	BI422991	BI422991 BI422991
C 269	37	4.3	677	13	BI490413	BI490413 603031660	C 341	36	4.2	155	12	BE964614	BE964614 601658540
C 270	37	4.3	717	10	AV716471	AV716471	C 342	36	4.2	155	13	BI330298	BI330298 BI330298
C 271	37	4.3	720	12	BG289378	BG289378 602381405	C 343	36	4.2	155	13	BI365336	BI365336 BI365336
C 272	37	4.3	732	12	BG114012	BG114012 602284496	C 344	36	4.2	155	13	BI365330	BI365330 BI365330
C 273	37	4.3	738	12	BF300482	BF300482 602031614	C 345	36	4.2	155	13	BI393309	BI393309 BI393309
C 274	37	4.3	742	13	BI490154	BI490154 603031905	C 346	36	4.2	155	13	BI426387	BI426387 BI426387
275	37	4.3	744	11	AY106416	AY106416 Zea may	C 347	36	4.2	155	17	N97520	N97520 0620W3 gmbP
276	37	4.3	774	10	AV755874	AV755874	C 348	36	4.2	156	13	BI333618	BI333618 BI333618
277	37	4.3	805	13	BI091593	BI091593 6026859015	C 349	36	4.2	156	13	BI369364	BI369364 BU425228
278	37	4.3	822	12	BF970631	BF970631 602273968	C 350	36	4.2	157	13	BI022366	BI022366 CM3-WT034
279	37	4.3	826	13	BI832817	BI832817 603082632	C 351	36	4.2	157	13	BI334481	BI334481 BI334481
C 280	37	4.3	937	17	CNS0068T	AL065880 Drosoph11	C 352	36	4.2	157	13	BI335390	BI335390 BI335390
C 281	37	4.3	1034	12	BE962970	BE962970 601656332	C 353	36	4.2	157	13	BI367353	BI367353 BI367353
C 282	37	4.3	1213	10	BE420722	BE420722 HMM001.H0	C 354	36	4.2	157	13	BI368954	BI368954 BI368954
C 283	37	4.3	1250	13	BI489117	BI489117 603021186	C 355	36	4.2	157	13	BI393595	BI393595 BI393595
C 284	37	4.3	1258	12	BE955891	BE955891 601659056	C 356	36	4.2	157	13	BI394883	BI394883 BI394883
C 285	37	4.3	1284	12	BI519336	BI519336 603062208	C 357	36	4.2	158	13	BI335804	BI335804 BI335804
C 286	37	4.3	1304	12	BE967292	BE967292 601661162	C 358	36	4.2	158	13	BI365086	BI365086 BI365086
C 287	37	4.3	1324	12	BE732599	BE732599 601571156	C 359	36	4.2	158	13	BI366675	BI366675 BI366675
C 288	37	4.3	1387	12	BF316629	BF316629 601903179	C 360	36	4.2	158	13	BI367046	BI367046 BI367046
C 289	37	4.3	1474	12	BG261116	BG261116 602372746	C 361	36	4.2	158	13	BI368799	BI368799 BI368799
C 290	37	4.3	1589	12	BG419146	BG419146 602446384	C 362	36	4.2	158	13	BI396125	BI396125 BI396125
C 291	37	4.3	1625	12	BE963209	BE963209 601656826	C 363	36	4.2	159	13	BI330804	BI330804 BI330804
C 292	37	4.3	2025	12	BE963127	BE963127 601656929	C 364	36	4.2	159	13	BI331326	BI331326 BI331326
C 293	37	4.3	2182	12	BF981953	BF981953 602306101	C 365	36	4.2	159	13	BI336432	BI336432 BI336432
C 294	36	4.2	60	9	AA422440	AA422440 vti12d02.s	C 366	36	4.2	159	13	BI365763	BI365763 BI365763
C 295	36	4.2	87	13	BI495570	BI495570 dfl1b09.	C 367	36	4.2	159	13	BI394806	BI394806 BI394806
C 296	36	4.2	88	9	AU261695	AU261695	C 368	36	4.2	159	13	BI424253	BI424253 BI424253
C 297	36	4.2	100	12	BF815228	BF815228 MR2-CT012	C 369	36	4.2	160	13	BE965724	BE965724 601659783
C 298	36	4.2	105	10	AW091417	AW091417 683023E11	C 370	36	4.2	160	12	BO332589	BO332589 BO332589

372	C	372	4.2	160	13	BJ334258	BJ334258	C	445	228	14	B0527688	B0527688
373	C	373	4.2	160	13	BJ334258	BJ334258	C	445	229	10	AM600647	AM600647
374	C	374	4.2	161	13	BJ334258	BJ334258	C	447	229	12	BF192242	BF192242
375	C	375	4.2	166	14	BQ389420	BQ389420	C	448	230	13	EM030846	EM030846
376	C	376	4.2	169	13	BQ389420	BQ389420	C	449	231	9	AU263276	AU263276
377	C	377	4.2	170	13	BQ389420	BQ389420	C	450	231	13	BI746763	BI746763
378	C	378	4.2	171	13	BQ389420	BQ389420	C	451	231	17	CNS03D27	CNS03D27
379	C	379	4.2	171	13	BQ389420	BQ389420	C	452	232	13	N98035	N98035
380	C	380	4.2	172	13	BQ389420	BQ389420	C	453	233	14	BQ339101	BQ339101
381	C	381	4.2	173	9	AL640567	AL640567	C	454	234	14	BM874445	BM874445
382	C	382	4.2	174	10	AV962602	AV962602	C	455	235	10	AM129604	AM129604
383	C	383	4.2	174	10	AM187209	AM187209	C	456	236	13	BI744868	BI744868
384	C	384	4.2	177	13	BQ394702	BQ394702	C	457	240	13	BM506431	BM506431
385	C	385	4.2	178	9	AL588434	AL588434	C	458	241	9	AL686546	AL686546
386	C	386	4.2	179	12	BQ327446	BQ327446	C	459	245	12	BG001306	BG001306
387	C	387	4.2	180	13	BI894908	BI894908	C	460	245	13	BM154504	BM154504
388	C	388	4.2	180	13	BI894908	BI894908	C	461	247	9	AT080087	AT080087
389	C	389	4.2	180	13	BM091809	BM091809	C	462	248	14	BM889429	BM889429
390	C	390	4.2	181	13	BQ933681	BQ933681	C	463	249	12	BF722381	BF722381
391	C	391	4.2	183	12	BF923395	BF923395	C	464	250	10	AM187451	AM187451
392	C	392	4.2	184	9	AL666430	AL666430	C	465	250	12	BG736841	BG736841
393	C	393	4.2	184	10	AM458261	AM458261	C	466	250	10	BM900253	BM900253
394	C	394	4.2	184	12	BE904911	BE904911	C	467	251	9	AA911635	AA911635
395	C	395	4.2	184	14	C84800	C84800	C	468	257	9	AT144850	AT144850
396	C	396	4.2	185	9	AL567883	AL567883	C	469	257	12	BG237821	BG237821
397	C	397	4.2	185	13	AL835829	AL835829	C	470	257	14	BQ666875	BQ666875
398	C	398	4.2	186	14	BQ567326	BQ567326	C	471	258	14	BM881955	BM881955
399	C	399	4.2	188	9	AL640991	AL640991	C	472	259	14	N97931	N97931
400	C	400	4.2	188	13	BQ330659	BQ330659	C	473	261	14	BM896676	BM896676
401	C	401	4.2	189	13	BI315626	BI315626	C	474	262	13	BI745508	BI745508
402	C	402	4.2	189	13	BM143922	BM143922	C	475	265	9	AU262271	AU262271
403	C	403	4.2	190	13	BQ739553	BQ739553	C	476	265	13	BM186101	BM186101
404	C	404	4.2	191	14	AA586749	AA586749	C	477	266	13	BI863396	BI863396
405	C	405	4.2	193	12	BF916550	BF916550	C	478	267	12	AM301863	AM301863
406	C	406	4.2	193	12	BF916550	BF916550	C	479	267	12	BG736549	BG736549
407	C	407	4.2	194	17	CNS072MX	CNS072MX	C	480	268	14	BM774871	BM774871
408	C	408	4.2	196	9	AL836066	AL836066	C	481	269	12	BF753033	BF753033
409	C	409	4.2	199	13	BQ333894	BQ333894	C	482	270	9	AL661209	AL661209
410	C	410	4.2	200	12	BG606920	BG606920	C	483	274	10	BE233379	BE233379
411	C	411	4.2	201	9	AA151109	AA151109	C	484	274	13	BM181089	BM181089
412	C	412	4.2	202	10	BE255229	BE255229	C	485	276	14	C84796	C84796
413	C	413	4.2	202	13	BQ333902	BQ333902	C	486	276	13	BQ395509	BQ395509
414	C	414	4.2	203	13	BQ330915	BQ330915	C	487	278	14	BM880671	BM880671
415	C	415	4.2	203	13	BQ330915	BQ330915	C	488	279	10	BE033059	BE033059
416	C	416	4.2	203	13	BQ330921	BQ330921	C	489	280	13	BM531944	BM531944
417	C	417	4.2	203	13	BQ333375	BQ333375	C	490	282	12	BG736615	BG736615
418	C	418	4.2	203	13	BI866976	BI866976	C	491	282	13	BI902697	BI902697
419	C	419	4.2	204	12	BQ237154	BQ237154	C	492	284	12	BI745476	BI745476
420	C	420	4.2	204	13	BQ333273	BQ333273	C	493	285	13	BF965814	BF965814
421	C	421	4.2	205	14	BQ629820	BQ629820	C	494	287	12	BI268512	BI268512
422	C	422	4.2	206	9	AL718325	AL718325	C	495	288	13	BI863466	BI863466
423	C	423	4.2	207	13	BM635418	BM635418	C	496	288	14	BQ527692	BQ527692
424	C	424	4.2	208	10	BE056103	BE056103	C	497	289	13	AL660133	AL660133
425	C	425	4.2	209	13	BM087314	BM087314	C	498	289	10	AM429843	AM429843
426	C	426	4.2	210	9	AL640398	AL640398	C	499	290	13	BI745120	BI745120
427	C	427	4.2	210	12	BF069697	BF069697	C	500	290	13	BQ640732	BQ640732
428	C	428	4.2	211	13	BI321301	BI321301	C	501	291	14	BI408847	BI408847
429	C	429	4.2	211	13	BI945109	BI945109	C	502	291	13	BI747245	BI747245
430	C	430	4.2	214	10	AM193975	AM193975	C	503	294	13	BM345035	BM345035
431	C	431	4.2	215	10	AM887457	AM887457	C	504	295	13	BG962133	BG962133
432	C	432	4.2	217	10	BE059127	BE059127	C	505	297	13	BG941170	BG941170
433	C	433	4.2	217	13	BI865874	BI865874	C	506	298	13	BM874445	BM874445
434	C	434	4.2	219	13	BI541562	BI541562	C	507	299	9	AL595093	AL595093
435	C	435	4.2	219	13	BI781603	BI781603	C	508	300	9	AL047039	AL047039
436	C	436	4.2	221	9	AL165384	AL165384	C	509	300	9	AL514717	AL514717
437	C	437	4.2	221	13	BQ953677	BQ953677	C	510	302	9	AL194884	AL194884
438	C	438	4.2	221	13	BI042928	BI042928	C	511	310	9	BM457790	BM457790
439	C	439	4.2	222	10	BM102605	BM102605	C	512	312	12	BM457790	BM457790
440	C	440	4.2	223	13	AM101889	AM101889	C	513	313	9	AT012928	AT012928
441	C	441	4.2	223	13	BI744972	BI744972	C	514	314	13	BM311810	BM311810
442	C	442	4.2	225	13	BM124451	BM124451	C	515	315	9	AL458190	AL458190
443	C	443	4.2	226	14	BM896662	BM896662	C	516	315	12	BG178237	BG178237
444	C	444	4.2	228	13	BG993456	BG993456	C	517	315	12	BG736327	BG736327

518	36	4.2	316	10	AM597643	AM597643 sj49a06.y	591	36	4.2	394	12	BE749870	BE749870 200930 MA
519	36	4.2	316	14	BO637699	BO637699 hel3d12.x	592	36	4.2	394	14	BM685815	BM685815 UI-E-CKO-
520	36	4.2	318	10	AM194282	AM194282 xmoa0c10.y	593	36	4.2	394	14	BM889036	BM889036 kb04e06.y
521	36	4.2	318	10	BE059034	BE059034 sn24c12.y	594	36	4.2	396	9	AI016656	AI016656 om96a04.x
522	36	4.2	320	12	BG629409	BG629409 CC-BEFLCL	595	36	4.2	401	9	AI479904	AI479904 cm70g08.x
523	36	4.2	321	9	AU032470	AU032470 AU032470	596	36	4.2	402	9	AI395109	AI395109 MA002437.
524	36	4.2	321	12	BF159593	BF159593 601769091	597	36	4.2	402	9	AI885920	AI885920 AL796651
525	36	4.2	322	13	BI509013	BI509013 BB170009A	598	36	4.2	403	13	BG953673	BG953673 CM4-CT016
526	36	4.2	323	14	AT001084	AT001084 AT001084	599	36	4.2	403	13	BI049924	BI049924 CM4-OT016
527	36	4.2	323	14	BM880723	BM880723 fd17e11.y	600	36	4.2	403	13	BM023352	BM023352 1e79c10.y
528	36	4.2	325	9	AA490112	AA490112 ab02e04.s	601	36	4.2	404	13	BM356985	BM356985 1e1-d2.TC
529	36	4.2	326	9	AU092544	AU092544 AU092544	602	36	4.2	408	17	AZ928338	AZ928338 479.dIF08
530	36	4.2	327	10	AM633107	AM633107 b103h04.x	603	36	4.2	410	9	AI793599	AI793599 C15105
531	36	4.2	327	14	BQ392654	BQ392654 NISC mq25	604	36	4.2	410	14	AI793599	AI793599 C15105
532	36	4.2	328	13	AA764860	AA764860 n261c03.s	605	36	4.2	411	10	BM781202	BM781202 AI297783
533	36	4.2	328	13	BI338114	BI338114 361783 MA	606	36	4.2	411	10	BM781202	BM781202 AI297783
534	36	4.2	333	13	BG671750	BG671750 DRNEXD05	607	36	4.2	412	9	AI297783	AI297783 BM393282
535	36	4.2	333	13	BM568122	BM568122 sak99d10.	608	36	4.2	412	9	AI297783	AI297783 BM393282
536	36	4.2	334	14	BQ100126	BQ100126 ph72g08.y	609	36	4.2	412	13	BM393282	BM393282 BM085810
537	36	4.2	334	17	AQ676101	AQ676101 HS 5501 B	610	36	4.2	416	9	AA085810	AA085810 BM114951
538	36	4.2	335	9	AI220836	AI220836 q907c09.x	611	36	4.2	416	13	BM114951	BM114951 CMS02AH7
539	36	4.2	336	14	BM801080	BM801080 AGENCOURT	612	36	4.2	417	17	CMS02AH7	CMS02AH7 BM608865
540	36	4.2	338	9	AU261877	AU261877 AU261877	613	36	4.2	418	13	BM114951	BM114951 CMS01ZGB
541	36	4.2	342	14	BQ099940	BQ099940 dh70c08.y	614	36	4.2	421	17	BM030865	BM030865 BM507504
542	36	4.2	343	9	AI662542	AI662542 mc15h06.x	615	36	4.2	424	13	BM507504	BM507504 BM558147
543	36	4.2	345	9	AI894196	AI894196 mc78c01.x	616	36	4.2	427	10	BM558147	BM558147 AV707923
544	36	4.2	346	12	BG783849	BG783849 SEADMC003	617	36	4.2	434	9	AI437804	AI437804 AV707923
545	36	4.2	346	13	BM356276	BM356276 kx61h02.y	618	36	4.2	436	10	AU263204	AU263204 BE878789
546	36	4.2	349	14	BQ448961	BQ448961 CNEST453	619	36	4.2	437	12	BE878789	BE878789 BM529056
547	36	4.2	350	9	AA815020	AA815020 oa88a09.s	620	36	4.2	437	13	BM529056	BM529056 UI-M-CE0-
548	36	4.2	350	9	AI147037	AI147037 qa82c07.x	621	36	4.2	438	13	BM529056	BM529056 UI-M-CE0-
549	36	4.2	350	9	AL595503	AL595503 AL595503	622	36	4.2	442	14	BQ299736	BQ299736 CM4-KN001
550	36	4.2	352	12	BF904247	BF904247 MR3-MT032	623	36	4.2	444	14	BM299736	BM299736 BI944215
551	36	4.2	353	13	BI744697	BI744697 rK91c06.y	624	36	4.2	446	14	BI944215	BI944215 sa92b11.y
552	36	4.2	353	9	AA629768	AA629768 ae63d10.s	625	36	4.2	446	14	BI944215	BI944215 sa92b11.y
553	36	4.2	356	9	AI769328	AI769328 wg36f06.x	626	36	4.2	447	10	BE038744	BE038744 AB06C02 A
554	36	4.2	356	13	BI424252	BI424252 sah67E01.	627	36	4.2	447	10	BE038744	BE038744 AB06C02 A
555	36	4.2	356	13	BM565211	BM565211 ih39c01.y	628	36	4.2	448	12	BE038744	BE038744 AB06C02 A
556	36	4.2	357	12	BG663614	BG663614 DRRAALC07	629	36	4.2	448	13	BM134794	BM134794 WHE0453-G
557	36	4.2	358	10	AM669118	AM669118 112295 MA	630	36	4.2	449	10	BE442733	BE442733 WHE1105-D
558	36	4.2	358	12	BG652938	BG652938 sad01h07.	631	36	4.2	449	14	C91154	C91154 C91154 Dict
559	36	4.2	359	9	AI458732	AI458732 tj37e09.x	632	36	4.2	450	9	AA190985	AA190985 zp85g10.s
560	36	4.2	360	9	AL799082	AL799082 AL799082	633	36	4.2	452	14	BQ520771	BQ520771 NISC n107
561	36	4.2	360	17	CNS04A3B	AL281360 Tetracodon	634	36	4.2	453	12	BQ662539	BQ662539 DRRAAE12
562	36	4.2	361	9	AL663475	AL663475 AL663475	635	36	4.2	453	13	BM277993	BM277993 As_Egz_51
563	36	4.2	363	10	AM541819	AM541819 C0149H07-	636	36	4.2	455	12	BM301653	BM301653 kt03g10.y
564	36	4.2	363	14	C90234	C90234 C90234 Dict	637	36	4.2	457	13	BM125312	BM125312 L0603B08-
565	36	4.2	366	9	AL514543	AL514543 AL514543	638	36	4.2	457	13	BQ945670	BQ945670 CM4-KN001
566	36	4.2	369	9	AL515389	AL515389 AL515389	639	36	4.2	459	9	AI436380	AI436380 t101c09.x
567	36	4.2	370	9	AA014418	AA014418 m16g911.x	640	36	4.2	460	14	R42667	R42667 y913a05.s1
568	36	4.2	371	9	AI653576	AI653576 tq96e05.x	641	36	4.2	460	9	AI181025	AI181025 ud74n06.x
569	36	4.2	371	9	AI318316	AI318316 AI318316	642	36	4.2	463	9	AL703354	AL703354 DXF2p6861
570	36	4.2	371	13	BM515033	BM515033 kj72f01.y	643	36	4.2	463	10	AV976393	AV976393 AV976393
571	36	4.2	374	9	AL044337	AL044337 DXF2p434A	644	36	4.2	464	9	AI318285	AI318285 AJ318285
572	36	4.2	374	10	AV723825	AV723825 AV723825	645	36	4.2	465	9	AI318285	AI318285 AJ318285
573	36	4.2	374	14	BQ385824	BQ385824 NISC mm14	646	36	4.2	466	13	BI944967	BI944967 sb03e07.y
574	36	4.2	375	9	AA708335	AA708335 zq07e01.s	647	36	4.2	468	10	AV717525	AV717525 AV717525
575	36	4.2	376	9	AI220834	AI220834 q907c07.x	648	36	4.2	468	13	BI534636	BI534636 BI534636
576	36	4.2	378	10	AM395009	AM395009 fb38c12.y	649	36	4.2	469	9	AU075713	AU075713 AU075713
577	36	4.2	379	13	BI079131	BI079131 602873422	650	36	4.2	470	9	AU263029	AU263029 AU263029
578	36	4.2	381	9	AL024005	AL024005 K8224b23	651	36	4.2	470	9	AU263029	AU263029 AU263029
579	36	4.2	383	9	AL1719429	AL1719429 AL1719429	652	36	4.2	474	13	BI738206	BI738206 ME8311-B1
580	36	4.2	383	9	AI334191	AI334191 qp92c12.x	653	36	4.2	475	12	BG842464	BG842464 ME8311-B1
581	36	4.2	384	9	AI061173	AI061173 an25c09.x	654	36	4.2	476	17	CNS02YX3M	CNS02YX3M AL219173
582	36	4.2	385	12	BG113373	BG113373 602284981	655	36	4.2	477	17	AA550666	AA550666 n220D06.s
583	36	4.2	388	13	BI895413	BI895413 ERESSTe38	656	36	4.2	479	9	AT002581	AT002581 AT002581
584	36	4.2	388	14	BM774308	BM774308 ra31h07.y	657	36	4.2	479	9	AU095274	AU095274 AU095274
585	36	4.2	390	17	CNS025HD	AL182074 Tetracodon	658	36	4.2	479	12	BG261785	BG261785 AU077487
586	36	4.2	391	9	AU263307	AU263307 AU263307	659	36	4.2	480	9	AU077487	AU077487 AU077487
587	36	4.2	392	9	AL514511	AL514511 AL514511	660	36	4.2	480	12	BG671339	BG671339 DRNBP08
588	36	4.2	392	13	BI697571	BI697571 603348738	661	36	4.2	481	12	BF535232	BF535232 602054296
589	36	4.2	393	10	AM231676	AM231676 687018D06	662	36	4.2	481	12	BF535232	BF535232 602054296
590	36	4.2	394	10	AV693913	AV693913 AV693913	663	36	4.2	482	14	BQ582233	BQ582233 1114d03.x

C 664	36	4.2	483	17	AA550010	AA550010 1089m3 gm	C 737	36	4.2	650	10	AW215874	AW215874 up02e02.x
C 665	36	4.2	484	17	AA15461	AA15461 mc58a02.x	C 738	36	4.2	650	14	C23659	C23659 C23659 Dict
C 666	36	4.2	484	17	AA550000	AA550000 1079m3 gm	C 739	36	4.2	653	9	AL520584	AL520584 AL520584 Dict
C 667	36	4.2	487	10	AA229259	AA229259 u008e02.y	C 740	36	4.2	654	9	AL732282	AL732282 AL732282
C 668	36	4.2	493	10	BI964855	BI964855 1e57e10.y	C 741	36	4.2	663	10	BI525891	BI525891 up02f01.x
C 669	36	4.2	493	10	AV956535	AV956535 AV956535	C 742	36	4.2	664	13	BI522894	BI522894 BI522894
C 670	36	4.2	494	13	BM380421	BM380421 MEST19-F	C 743	36	4.2	665	17	CNS0421A	CNS0421A CNS0421A
C 671	36	4.2	494	13	BO841769	BO841769 WHE2985-A	C 744	36	4.2	673	17	AG150663	AG150663 Pan trogl
C 672	36	4.2	495	13	BM563321	BM563321 AGENCOUT	C 745	36	4.2	674	11	BC018428	BC018428 Homo sapi
C 673	36	4.2	497	13	BM380954	BM380954 MEST127-G	C 746	36	4.2	683	12	BF452876	BF452876 AV682476
C 674	36	4.2	501	14	BO525537	BO525537 NISC_nol1	C 747	36	4.2	686	14	C93771	C93771 C93771 Dict
C 675	36	4.2	502	17	AO882566	AO882566 HS_5407-B	C 748	36	4.2	689	17	CNS04AB8	CNS04AB8 CNS04AB8
C 676	36	4.2	504	9	AI436864	AI436864 fd34d12.x	C 749	36	4.2	695	14	C93772	C93772 C93772 Dict
C 677	36	4.2	506	10	AM55184	AM55184 10251B02-	C 750	36	4.2	700	12	EG026194	EG026194 EG026194
C 678	36	4.2	513	14	R20548	BF781707 602104230	C 751	36	4.2	703	13	BI087461	BI087461 602851091
C 679	36	4.2	513	17	BH511474	BH511474 yf57f08_81	C 752	36	4.2	707	9	AO077474	AO077474 AO077474
C 680	36	4.2	517	14	R37390	R37390 yf77f06_81	C 753	36	4.2	707	17	BH567037	BH567037 BOXD0567F
C 681	36	4.2	521	17	CNS022PX	AL221262 Tetradon	C 754	36	4.2	710	17	AG040865	AG040865 Pan trogl
C 682	36	4.2	521	17	CNS022PX	AL221262 Tetradon	C 755	36	4.2	711	10	BE534359	BE534359 BE534359
C 683	36	4.2	523	14	AO262124	AO262124 NISC_ff15	C 756	36	4.2	711	10	AY068531	AY068531 Schmdldea
C 684	36	4.2	523	14	BO267877	BO267877 NISC_ff15	C 757	36	4.2	720	12	BG289378	BG289378 602381405
C 685	36	4.2	529	12	BE878764	BE878764 601493030	C 758	36	4.2	721	13	BJ384615	BJ384615 BJ384615
C 686	36	4.2	529	12	BF128553	BF128553 601810801	C 759	36	4.2	724	9	AL721250	AL721250 AL721250
C 687	36	4.2	529	14	C99537	C99537 C99537 Rice	C 760	36	4.2	724	14	BO796998	BO796998 EST 5936
C 688	36	4.2	533	14	BM938298	BM938298 UI-M-BZL-	C 761	36	4.2	725	10	AM332539	AM332539 S9P6 AGS-
C 689	36	4.2	537	9	AL514397	AL514397 AL514397	C 762	36	4.2	736	13	BI489164	BI489164 BI489164
C 690	36	4.2	537	9	BI000365	BI000365 MR3-HN006	C 763	36	4.2	736	13	BI489164	BI489164 BI489164
C 691	36	4.2	537	9	BO746528	BO746528 UI-M-FAO-	C 764	36	4.2	745	17	AA392077	AA392077 LDI1555.5
C 692	36	4.2	541	12	BG623042	BG623042 602647924	C 765	36	4.2	745	17	AO234504	AO234504 m9b001BL
C 693	36	4.2	542	14	BO389705	BO389705 NISC_m009	C 766	36	4.2	750	12	BG261362	BG261362 602373135
C 694	36	4.2	544	13	BM422094	BM422094 V024D01 O	C 767	36	4.2	753	12	BF742324	BF742324 602631478
C 695	36	4.2	545	13	BI654947	BI654947 603833208	C 768	36	4.2	753	12	BF629311	BF629311 601771184
C 696	36	4.2	547	12	BF579015	BF579015 602096134	C 769	36	4.2	756	13	BI524047	BI524047 HVSMED001
C 697	36	4.2	550	9	AU263167	AU263167 AU263167	C 770	36	4.2	756	12	BG568336	BG568336 602587290
C 698	36	4.2	554	14	BM320510	BM320510 NISC_n105	C 771	36	4.2	761	17	BG568336	BG568336 602587290
C 699	36	4.2	555	13	BM394602	BM394602 50072-2-4	C 772	36	4.2	765	17	BH148938	BH148938 ENTPE527F
C 700	36	4.2	560	14	BO798516	BO798516 EST 685 G	C 773	36	4.2	778	12	BG740883	BG740883 602633775
C 701	36	4.2	560	14	BO799688	BO799688 EST 1857	C 774	36	4.2	778	12	AG058583	AG058583 Pan trogl
C 702	36	4.2	563	14	BO522774	BO522774 NISC_n118	C 775	36	4.2	785	12	BG288001	BG288001 602387778
C 703	36	4.2	564	14	BO394823	BO394823 NISC_n118	C 776	36	4.2	804	13	BI490367	BI490367 603031831
C 704	36	4.2	567	9	AL511470	AL511470 AL511470	C 777	36	4.2	805	12	BG392282	BG392282 602410446
C 705	36	4.2	567	9	AL511470	AL511470 AL511470	C 778	36	4.2	812	17	AG044252	AG044252 Pan trogl
C 706	36	4.2	569	13	BM269209	BM269209 MEST1406-G	C 779	36	4.2	819	13	BM397721	BM397721 5009-0-36
C 707	36	4.2	572	14	C90451	C90451 C90451 Dict	C 780	36	4.2	821	9	AA987044	AA987044 uc77e12.x
C 708	36	4.2	574	13	BI523033	BI523033 603175528	C 781	36	4.2	821	10	AV758661	AV758661 AV758661
C 709	36	4.2	576	14	BM939047	BM939047 UI-M-BZL-	C 782	36	4.2	821	12	BF383726	BF383726 602044634
C 710	36	4.2	582	11	AY109035	AY109035 Zee mayB	C 783	36	4.2	826	12	BG619471	BG619471 602618839
C 711	36	4.2	584	9	AA075221	AA075221 zm87f03.s	C 784	36	4.2	836	12	BG029912	BG029912 602297256
C 712	36	4.2	585	14	BO523814	BO523814 NISC_n001	C 785	36	4.2	837	9	AI255435	AI255435 u158605.x
C 713	36	4.2	586	12	BF782515	BF782515 602106531	C 786	36	4.2	847	13	BI734120	BI734120 603352085
C 714	36	4.2	588	14	BO526974	BO526974 NISC_n019	C 787	36	4.2	847	17	CNS0257Y	CNS0257Y CNS0257Y
C 715	36	4.2	588	14	BO388777	BO388777 NISC_m003	C 788	36	4.2	848	17	BG870832	BG870832 Tetradon
C 716	36	4.2	596	9	AU263101	AU263101 AU263101	C 789	36	4.2	858	12	BG870832	BG870832 Tetradon
C 717	36	4.2	599	14	BO251019	BO251019 TAP25034B	C 790	36	4.2	862	12	BE970652	BE970652 601497967
C 718	36	4.2	601	9	AU262588	AU262588 AU262588	C 791	36	4.2	869	12	BE970652	BE970652 601497967
C 719	36	4.2	602	13	BI868789	BI868789 603391944	C 792	36	4.2	889	13	BE884698	BE884698 602994752
C 720	36	4.2	603	14	C24400	C24400 C24400 Dict	C 793	36	4.2	895	12	BE884698	BE884698 602994752
C 721	36	4.2	604	9	AU261895	AU261895 AU261895	C 794	36	4.2	915	13	BM425365	BM425365 BM425365
C 722	36	4.2	606	13	BM079963	BM079963 MEST102-A	C 795	36	4.2	925	17	BI232833	BI232833 BI232833
C 723	36	4.2	608	14	BO522946	BO522946 NISC_n119	C 796	36	4.2	934	17	BH164537	BH164537 ENTQ16TF
C 724	36	4.2	610	14	BO393919	BO393919 PFRSTab4	C 797	36	4.2	936	12	BG682316	BG682316 602629635
C 725	36	4.2	613	17	AO922590	AO922590 RPT-23-2	C 798	36	4.2	939	17	CNS01UPU	CNS01UPU CNS01UPU
C 726	36	4.2	614	17	CNS0152H	AL104915 Drosophill	C 799	36	4.2	940	17	CNS046PD	CNS046PD CNS046PD
C 727	36	4.2	615	14	C25773	C25773 C25773 Dict	C 800	36	4.2	950	10	BE039592	BE039592 OC01E10 O
C 728	36	4.2	619	12	AL514935	AL514935 AL514935	C 801	36	4.2	957	12	BE731649	BE731649 BE731649
C 729	36	4.2	619	12	BE844577	BE844577 EST322 AP	C 802	36	4.2	964	17	CNS00590	CNS00590 CNS00590
C 730	36	4.2	621	12	BF107957	BF107957 601823986	C 803	36	4.2	978	17	AL549668	AL549668 Tetradon
C 731	36	4.2	622	14	BO524805	BO524805 NISC_n007	C 804	36	4.2	979	9	AL549668	AL549668 Tetradon
C 732	36	4.2	623	14	BO391283	BO391283 NISC_nq17	C 805	36	4.2	980	17	BI489205	BI489205 603021472
C 733	36	4.2	626	11	AY068430	AY068430 Schmdldea	C 806	36	4.2	983	13	BI489205	BI489205 603021472
C 734	36	4.2	630	17	BO524081	BO524081 NISC_n002	C 807	36	4.2	989	17	AZ549932	AZ549932 ENTPE67F
C 735	36	4.2	637	17	CNS0245B	AL180344 Tetradon	C 808	36	4.2	1012	14	BO939005	BO939005 BO939005
C 736	36	4.2	643	9	AU262240	AU262240 AU262240	C 809	36	4.2	1024	12	BF792715	BF792715 BF792715

C 810	36	4.2	1027	17	AZ167189	C 883	35	4.1	121	14	H74729	H74729 274 Deletio
C 811	36	4.2	1040	13	B1521877	884	35	4.1	122	14	BQ235651	BQ235651 hdb3n09.g
C 812	36	4.2	1051	9	AL524212	885	35	4.1	125	13	B111806	B111806 602897836
C 813	36	4.2	1059	12	BF183554	886	35	4.1	126	10	AV961814	AV961814 AV961814
C 814	36	4.2	1064	17	CNS02DX4	887	35	4.1	126	10	AM426501	AM426501 60745 MAR
C 815	36	4.2	1095	12	BF525514	888	35	4.1	126	13	B1743529	B1743529 kx51d12.y
C 816	36	4.2	1100	11	BC016864	889	35	4.1	129	14	C90008	C90008 C90008 Dict
C 817	36	4.2	1101	13	B1489094	C 890	35	4.1	130	9	AL370359	AL370359 McBA37C10
C 818	36	4.2	1101	17	CNS003B4	891	35	4.1	132	2	AA607405	AA607405 vo3jF09.x
C 819	36	4.2	1101	17	CNS000JP	892	35	4.1	135	12	BE874706	BE874706 601485832
C 820	36	4.2	1101	17	CNS00Y6	893	35	4.1	137	12	BE672397	BE672397 602150637
C 821	36	4.2	1101	17	CNS0171F	894	35	4.1	137	12	BE976640	BE976640 b554b03.y
C 822	36	4.2	1112	12	BG116078	895	35	4.1	137	13	BE956252	BE956252 QV1 -CT075
C 823	36	4.2	1112	13	BO952170	896	35	4.1	139	9	AA743474	AA743474 ny13F09.s
C 824	36	4.2	1117	13	BM415411	897	35	4.1	139	9	AA129387	AA129387 qc34d08.x
C 825	36	4.2	1145	13	B1521872	898	35	4.1	140	9	AI140633	AI140633 lb32b08.x
C 826	36	4.2	1147	13	B149110	899	35	4.1	142	9	AI262222	AI262222 qk09e09.x
C 827	36	4.2	1150	12	BG532790	900	35	4.1	143	9	AA189259	AA189259 mc89a03.x
C 828	36	4.2	1162	12	BE966022	C 901	35	4.1	143	13	BE988379	BE988379 MR3-HT120
C 829	36	4.2	1164	12	B1524383	C 902	35	4.1	144	9	AL502847	AL502847 AL502847
C 830	36	4.2	1165	13	B1522984	C 903	35	4.1	144	12	BF751315	BF751315 RC3-BN042
C 831	36	4.2	1175	13	BE421167	C 904	35	4.1	145	10	AM949205	AM949205 QV4-FT000
C 832	36	4.2	1175	13	BE421167	C 905	35	4.1	146	9	AU072297	AU072297 AU072297
C 833	36	4.2	1203	13	CNS00ZM1	906	35	4.1	146	13	BI941674	BI941674 sc84a11.y
C 834	36	4.2	1203	13	BM466037	907	35	4.1	147	12	BE165052	BE165052 602343436
C 835	36	4.2	1265	14	BE967005	908	35	4.1	147	13	BG991133	BG991133 MR2-HT118
C 836	36	4.2	1269	13	BE964449	909	35	4.1	148	9	AA289204	AA289204 vb33f01.x
C 837	36	4.2	1270	13	BG964449	C 910	35	4.1	148	12	BE874133	BE874133 601484317
C 838	36	4.2	1375	13	B1523146	C 911	35	4.1	149	9	AI439814	AI439814 c156d06.x
C 839	36	4.2	1392	12	BG030520	C 912	35	4.1	149	13	BI744597	BI744597 rk89a05.y
C 840	36	4.2	1434	13	B1524419	C 913	35	4.1	151	13	BI268634	BI268634 NF014A11G
C 841	36	4.2	1475	13	B1524374	C 914	35	4.1	151	13	BI002433	BI002433 MR3-HN015
C 842	36	4.2	1553	13	B1524338	C 915	35	4.1	153	12	BE874163	BE874163 601484347
C 843	36	4.2	1563	12	BG763366	C 916	35	4.1	155	10	BE232007	BE232007 1362909 MA
C 844	36	4.2	1613	10	BE616058	917	35	4.1	156	9	AA036486	AA036486 mh17F09.x
C 845	36	4.2	1657	12	BE964263	918	35	4.1	157	9	AU071392	AU071392 AU071392
C 846	36	4.2	1759	12	BG681855	919	35	4.1	160	9	AU175799	AU175799 AU175799
C 847	36	4.2	1819	11	BC031681	C 920	35	4.1	160	13	BI001154	BI001154 MR3-HN012
C 848	36	4.2	1996	11	BC013320	C 921	35	4.1	161	9	AL386476	AL386476 McBC34H06
C 849	36	4.2	4195	11	BC021044	C 922	35	4.1	161	9	AU095555	AU095555 AU095555
C 850	35	4.1	4195	9	AI431439	C 923	35	4.1	162	9	AL726422	AL726422 AL726422
C 851	35	4.1	56	14	BQ520931	C 924	35	4.1	162	13	BI268676	BI268676 NF021H04G
C 852	35	4.1	57	13	BI743047	C 925	35	4.1	162	13	BM070725	BM070725 sak31904.x
C 853	35	4.1	58	10	AV954391	C 926	35	4.1	164	13	BG991137	BG991137 MR2-HT118
C 854	35	4.1	58	14	BQ521646	C 927	35	4.1	164	13	BI095172	BI095172 sae04C06.
C 855	35	4.1	73	10	AV971432	C 928	35	4.1	165	9	AA265842	AA265842 m270g01.x
C 856	35	4.1	76	9	AA572761	C 929	35	4.1	165	10	AM101024	AM101024 sd64f11.y
C 857	35	4.1	93	14	BQ234257	C 930	35	4.1	165	12	BF535331	BF535331 602052106
C 858	35	4.1	93	14	BQ234543	C 931	35	4.1	165	13	BG950562	BG950562 PM0-CT070
C 859	35	4.1	93	14	BQ234543	C 932	35	4.1	165	13	BG977643	BG977643 MR2-CT018
C 860	35	4.1	93	14	BQ234543	C 933	35	4.1	166	14	BQ145504	BQ145504 NF009F12G
C 861	35	4.1	94	14	BQ788232	C 934	35	4.1	167	10	BE381058	BE381058 601271405
C 862	35	4.1	94	14	BQ788232	C 935	35	4.1	167	14	C99396	C99396 C99396 R1ce
C 863	35	4.1	100	13	BI024076	C 936	35	4.1	168	10	AM101810	AM101810 sd70g06.y
C 864	35	4.1	102	2	HSW003325	C 937	35	4.1	168	13	BG996101	BG996101 MR4-HT119
C 865	35	4.1	103	10	AV948612	C 938	35	4.1	169	9	AI932889	AI932889 w939c05.x
C 866	35	4.1	105	10	AV948612	C 939	35	4.1	169	9	AI964507	AI964507 436011H05
C 867	35	4.1	105	13	BI671965	C 940	35	4.1	169	9	AL037030	AL037030 DFE2P564H
C 868	35	4.1	106	2	HSW003326	C 941	35	4.1	169	9	AL037030	AL037030 DFE2P564H
C 869	35	4.1	106	14	C25768	C 942	35	4.1	169	12	BE896769	BE896769 601437442
C 870	35	4.1	107	12	BI611851	C 943	35	4.1	169	13	BG983805	BG983805 MR4-CN014
C 871	35	4.1	107	13	BI492602	C 944	35	4.1	169	13	BQ835013	BQ835013 Po ad 06B
C 872	35	4.1	110	12	BF771374	C 945	35	4.1	171	13	BG981076	BG981076 MR3-CN014
C 873	35	4.1	112	13	BQ788232	C 946	35	4.1	171	14	BM889264	BM889264 kb08a03.y
C 874	35	4.1	112	13	BQ826006	C 947	35	4.1	172	9	AU175838	AU175838 AU175838
C 875	35	4.1	113	13	BI367608	C 948	35	4.1	172	10	BI58078	BI58078 428454 MA
C 876	35	4.1	114	9	AI280525	C 949	35	4.1	173	13	BE482369	BE482369 168131 BA
C 877	35	4.1	116	9	AI280525	C 950	35	4.1	173	13	BI021161	BI021161 CM0-MT035
C 878	35	4.1	116	12	BF766531	C 951	35	4.1	173	13	BM620920	BM620920 170006874
C 879	35	4.1	117	14	BQ788368	C 952	35	4.1	174	9	AA504521	AA504521 aa60n12.s
C 880	35	4.1	118	14	BQ788245	C 953	35	4.1	174	13	BI002918	BI002918 MR3-HN015
C 881	35	4.1	119	10	AM431018	C 954	35	4.1	175	9	AI334890	AI334890 lb33a07.x
C 882	35	4.1	121	10	AM655414	C 955	35	4.1	175	9	AL043469	AL043469 DKF2p434A

956	35	4.1	175	10	AM119465
957	175	4.1	175	14	EM896455
958	35	4.1	175	14	BQ299084
959	35	4.1	176	12	BG653001
960	35	4.1	176	13	BG981095
961	35	4.1	176	13	BG991084
962	35	4.1	178	9	AU058315
963	35	4.1	179	9	A1874162
964	35	4.1	179	9	AU074259
965	35	4.1	179	13	B1042748
966	35	4.1	180	9	AU175646
967	35	4.1	181	9	A1567894
968	35	4.1	181	14	BQ826005
969	35	4.1	182	14	C93784
970	35	4.1	182	12	BG001253
971	35	4.1	183	10	AM898582
972	35	4.1	183	12	BG577746
973	35	4.1	184	10	AV993802
974	35	4.1	184	10	AM176457
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976	35	4.1	185	10	AM196138
977	35	4.1	185	12	BF811784
978	35	4.1	185	10	BE807445
979	35	4.1	185	13	BE101437
980	35	4.1	185	13	B1703945
981	35	4.1	185	14	BQ145479
982	35	4.1	186	9	AA796636
983	35	4.1	187	9	AU074867
984	35	4.1	187	14	BQ146233
985	35	4.1	187	14	C93857
986	35	4.1	188	10	BE519303
987	35	4.1	188	13	B1001827
988	35	4.1	188	17	AZ576647
989	35	4.1	189	10	AM164346
990	35	4.1	189	14	BQ577707
991	35	4.1	189	14	C92531
992	35	4.1	190	14	BM506342
993	35	4.1	190	13	BQ128687
994	35	4.1	191	13	BG956187
995	35	4.1	191	13	B1002366
996	35	4.1	191	13	B1695960
997	35	4.1	191	13	B1701585
998	35	4.1	191	13	B1747326
999	35	4.1	191	13	B1941625
1000	35	4.1	191	13	B1945299

ALIGNMENTS

RESULT 1	562 bp	mRNA	linear	EST 01-MAR-2002
BM732121	562 bp	mRNA	linear	EST 01-MAR-2002
LOCUS	562 bp	mRNA	linear	EST 01-MAR-2002
DEFINITION	562 bp	mRNA	linear	EST 01-MAR-2002
Accession	562 bp	mRNA	linear	EST 01-MAR-2002
Version	562 bp	mRNA	linear	EST 01-MAR-2002
Keywords	562 bp	mRNA	linear	EST 01-MAR-2002
Source	562 bp	mRNA	linear	EST 01-MAR-2002
Organism	562 bp	mRNA	linear	EST 01-MAR-2002
Reference	562 bp	mRNA	linear	EST 01-MAR-2002
Authors	562 bp	mRNA	linear	EST 01-MAR-2002
Title	562 bp	mRNA	linear	EST 01-MAR-2002

JOURNAL	Unpublished (1999)
COMMENT	Contact: Shoemaker R./Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu This clone is available through: Reggen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: cu@reggen.com web site: www.reggen.com Seq primer: -408P from Gibco High quality sequence stop: 421.
FEATURES	location/Qualifiers
source	1..562
	/organism="Glycine max"
	/db_xref="taxon:3847"
	/clone="SOYBEAN CLONE ID: Gm-c1061-4678"
	/clone_id="Gm-c1061"
	/tissue_type="mature flowers of field grown plants"
	/lab_host="RDH10B"
	/note="vector: pBluescript II SK+; Site_1: EcoRI, Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
BASE COUNT	187 a 115 c 128 g 132 t
ORIGIN	
Query Match	65.1%; Score 562; DB 14; Length 562;
Best Local Similarity	100.0%; Pred. No. 3.3e-128; Mismatches 0; Indels 0; Gaps 0;
Matches 562; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
10	CTATGACACACACAAAGTCAATGATTAATAAAACAAAGTGTAAAGCTCTCAAGATCTCGA 69
1	CTATGACACACACAAAGTCAATGATTAATAAAACAAAGTGTAAAGCTCTCAAGATCTCGA 60
70	AGTGAAGAAAGGCGCTTGACAAATGAAAGAAAGTCAATGATTAATAAAACAAAGTGTAAAGCTCTCGA 129
61	AGTGAAGAAAGGCGCTTGACAAATGAAAGAAAGTCAATGATTAATAAAACAAAGTGTAAAGCTCTCGA 120
130	TCATGAGGAGAGGTGTTGAACTCTTTGGCCAAAGCTGCTGCTCAACGTAACGGA 189
121	TCATGAGGAGAGGTGTTGAACTCTTTGGCCAAAGCTGCTGCTCAACGTAACGGA 180
190	GAGTGGCCGCTAAGGAGGCTTAATTAATTCCTCCGCTGATGTTGAAGAGGAATATAC 249
181	GAGTGGCCGCTAAGGAGGCTTAATTAATTCCTCCGCTGATGTTGAAGAGGAATATAC 240
250	ACCGAGGAAACAACTTTGATTTATGAGCTCCAGCAAGAGTGGGAAACAGTGGTCCA 309
241	ACCGAGGAAACAACTTTGATTTATGAGCTCCAGCAAGAGTGGGAAACAGTGGTCCA 300
310	AATGGCAAGCATCTACCTGGAAGAGCTGATTAATGAATCAAGAACTATTGAGGAGCAAG 369
301	AATGGCAAGCATCTACCTGGAAGAGCTGATTAATGAATCAAGAACTATTGAGGAGCAAG 360
370	GATTCAGAGCAATCAAGCAAGCTGAGAACTTTCAGCAACAGAGTATATATTCGA 429
361	GATTCAGAGCAATCAAGCAAGCTGAGAACTTTCAGCAACAGAGTATATATTCGA 420
430	GATTAAGATCAACAACTGACCTAGCCATGTTTCACCAATGCGTGAAGCCATGAGAT 489
421	GATTAAGATCAACAACTGACCTAGCCATGTTTCACCAATGCGTGAAGCCATGAGAT 480

QY 490 GTATTCACACCTGTGTATCAAGAAATGTAGAGCCATTTCACATCAGTTCCTACAT 549
 DB 481 GTATTCACACCTGTGTATCAAGAAATGTAGAGCCATTTCACATCAGTTCCTACAT 540
 QY 550 TAATCTGATCAATCCAGTTGT 571
 DB 541 TAATCTGATCAATCCAGTTGT 562

RESULT 2
 BE820766/c 586 bp mRNA linear EST 24-MAY-2001
LOCUS GM70001220H11 Gm-r1070 Glycine max cDNA clone Gm-r1070-4966 3',
 mRNA sequence.
ACCESSION BE820766
VERSION BE820766.1 GI:10253000
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 586)
 Vodka, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Coryell, V.,
 Erpelid, J., Rapp, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.
 A Functional Genomics Program for Soybean (NSF 9872565)
 Unpublished (1999)
 Other ESTs: AM459279 corresponding to Gm-cl016-5560 (5')
 Contact: Vodka, L.O., PI, A Functional Genomics Program for
 Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l-vodka@uiuc.edu
 This clone is available through: Genome Systems, Inc. 4633 World
 Parkway Circle St. Louis, Missouri 63134. For further information
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
 427-3324 or contact: clones@genomesystems.com or info@genome
 systems.com web site: www.genomesystems.com
 Seq primer: 5'-TTTTTTTTTTTTTTTTT (A/C/G)-3'.
FEATURES
source
 location/Qualifiers
 1..586
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="Gm-r1070-4966"
 /clone_1ib="Gm-r1070"
 /note="The library Gm-r1070 is a sequence-driven, rerecked
 set of 9,216 clones selected from cDNA libraries from
 various tissues and stages of development of soybean that
 represent 2,639 sequences from immature cotyledons, 1,770
 from immature seed coats, 3,938 from flowers, and 869
 from young pods. The 5' ESTs of the source clones from
 the different libraries was used to select singletons, or
 a representative of each contig, which were rerecked to
 form library Gm-r1070. The cDNA clones of the rerecked
 Gm-r1070 library were then sequenced at the 3' end. The
 contig analysis to select unique genes was performed by
 the laboratory of Ernest Retzel, Center for Computational
 Genomics and Bioinformatics, University of Minnesota,
 http://www.cbc.umn.edu/ResearchProjects/soybean/index.html
 . Rerecking was performed by Genome Systems, St. Louis,
 http://www.genomesystems.com, and 3' sequencing by the
 Keck Center for Comparative and Functional Genomics,
 University of Illinois,
 http://www.life.uiuc.edu/biotech/keck.html. Note: The
 corresponding 5' EST from each clone in the Gm-r1070
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can be
 obtained by referring to the Genome Systems clone ID of

the original cDNA library that is also listed under
 'OTHER EST'.
BASE COUNT 173 a 110 c 100 g 194 t 9 others
ORIGIN
 Query Match 42.9%; Score 370; DB 12; Length 586;
 Best Local Similarity 99.6%; Pred. No. 1,9e-81;
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 CCTGGAAGACGTATATATGATCAAGAACTATTTGGAGGACAGAGTCGAGACATC 385
 DB 583 CTTGGAAGACGTATATATGATCAAGAACTATTTGGAGGACAGAGTCGAGACATC 524
 QY 386 AACCAAGCTGAGAACTTTGACGACAGAGTAGTAATATTTGAGATAATGATCA 445
 DB 523 AACCAAGCTGAGAACTTTGACGACAGAGTAGTAATATTTGAGATAATGATCA 464
 QY 446 GCTAGCACTAGCAATGCTTTCACAGAGCTGAGCCATGAGATATATCTCA 505
 DB 463 GCTAGCACTAGCAATGCTTTCACAGAGCTGAGCCATGAGATATATCTCA 404
 QY 506 TATCAAGAAATGTAGAGCAATTTCACTCACTGCTTCTCAATTAATCCTGATCA 565
 DB 403 TATCAAGAAATGTAGAGCAATTTCACTCACTGCTTCTCAATTAATCCTGATCA 344
 QY 566 AGTTGTTGACCAATGACCAACCAACATTAATTAATGAGAGAGATAGCTGCA 625
 DB 343 AGTTGTTGACCAATGACCAACCAACATTAATTAATGAGAGATAGCTGCA 284
 QY 626 ATGCATTAATGACCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 685
 DB 283 ATGCATTAATGACCGGTATTAATTAATTAATTAATTAATTAATTAATTAAT 224
 QY 686 TAAGGCTGAATGCTGTGATTAATAACATTAATTAATTAATTAATTAATTAAT 745
 DB 223 TAAGGCTGAATGCTGTGATTAATAACATTAATTAATTAATTAATTAATTAAT 164
 QY 746 ATGTTGTTGTTGCGTACCAATTAATTAATTAATTAATTAATTAATTAAT 797
 DB 163 ATGTTGTTGTTGCGTACCAATTAATTAATTAATTAATTAATTAATTAAT 112

RESULT 3
 AM459279 431 bp mRNA linear EST 03-DEC-2001
LOCUS SH22H08.Y1 Gm-cl016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl016-5560 5' similar to TR:Q92TD5 Q92TD5 PUTATIVE TRANSCRIPTION
 FACTOR ; mRNA sequence.
ACCESSION AM459279
VERSION AM459279.1 GI:7029496
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 431)
 Shoemaker, R., Keim, P., Vodka, L., Erpelid, J., Coryell, V., Khanna,
 A., Bolla, B., Matra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wyle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
 Y., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
 R., Ritzer, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
 R., Waterson, R. and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 Contact: Shoemaker R/Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 723 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 411.

FEATURES

SOURCE:

1. 431
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-5560"
/clone_lib="Gm-c1016"
/tissue_type="Immature flowers of field grown plants"
/lab_host="XLI10-Gold"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 145 a 81 c 88 g 117 t

ORIGIN

Query Match 40.4%; Score 349; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.3e-76;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 326 CCTGGAAGCACTGATTAAGATCAAGAACTATTGAGAGCAAGATCCAGAACATC 385
Db 8 CTGGAAGCACTGATTAAGATCAAGAACTATTGAGAGCAAGATCCAGAACATC 67
QY 386 AAGCAAGTGAAGACTTTCAGCAACAGAGTAGTAATATTCTGAGATTAATGATCACC 445
Db 68 AAGCAAGTGAAGACTTTCAGCAACAGAGTAGTAATATTCTGAGATTAATGATCACC 127
QY 446 GCTAGCACTAGCCATGTTTCCACCATGGCTGAGCCATGAGATGATTTCTCCACCCTGT 505
Db 128 GCTAGCACTAGCCATGTTTCCACCATGGCTGAGCCATGAGATGATTTCTCCACCCTGT 187
QY 506 TATCAAGGATGTTAGAGCCATTTTCACTCACTGTTCCATTAATCTGATCAATCC 565
Db 188 TATCAAGGATGTTAGAGCCATTTTCACTCACTGTTCCATTAATCTGATCAATCC 247
QY 566 AATTGTTGACCAATGACCAACACATTAATTAATGAGCATGAGATAGCTGTCA 625
Db 248 AATTGTTGACCAATGACCAACACATTAATTAATGAGCATGAGATAGCTGTCA 307
QY 626 ATGCAATTAATGAAACGGTGATTAATATTATCAAGATTAATCACTAAGTT 674
Db 308 ATGCAATTAATGAAACGGTGATTAATATTATCAAGATTAATCACTAAGTT 356

RESULT 4
BE058947 450 bp mRNA linear EST 03-DEC-2001
LOCUS BE058947
DEFINITION sm23p01.y1 Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-12290 5', similar to TR:0927DS 0927DS PUTATIVE TRANSCRIPTION FACTOR 1, mRNA sequence.

ACCESSION BE058947
VERSION BE058947.1 GI:8403313
KEYWORDS EST.

SOURCE soybean.
ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE

AUTHORS

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 450)
Shoemaker R., Kelm P., Vodkin L., Erpelting J., Coryell V., Khanna A., Bolla B., Marra M., Hillier L., Kucaba T., Martin J., Beck C., Wylie T., Underwood K., Stepien M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R., Meterson R. and Wilson R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R./Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 411.

FEATURES

SOURCE

1. 450
Location/Qualifiers
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-12290"
/clone_lib="Gm-c1016"
/tissue_type="Immature flowers of field grown plants"
/lab_host="XLI10-Gold"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT 151 a 84 c 90 g 125 t

ORIGIN

Query Match 33.0%; Score 285; DB 10; Length 450;
Best Local Similarity 99.7%; Pred. No. 1.2e-60;
Matches 335; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 339 ATATGAGATCAAGACTATTGAGAGACAGATCCAGAGACATCAAGACCTGAGA 398
Db 36 ATATGAGATCAAGACTATTGAGAGACAGATCCAGAGACATCAAGACCTGAGA 95
QY 399 ACTTCAGCAACAGAGTAGTAATATTCTGAGATTAATGATCAGCACTAGACC 456
Db 96 ACTTCAGCAACAGAGTAGTAATATTCTGAGATTAATGATCAGCACTAGACC 155
QY 459 ATGTTTCCACCATGGCTGAGCCCATGAGATGATTTCTCCACCCTGTTATCAAGAAATGT 518
Db 156 ATGTTTCCACCATGGCTGAGCCCATGAGATGATTTCTCCACCCTGTTATCAAGAAATGT 215
QY 519 TAGAGCACTTTTCAACTAGTTCCTCAATTAATCTGATCAATCCAGTGTGTGACCA 578
Db 216 TAGAGCACTTTTCAACTAGTTCCTCAATTAATCTGATCAATCCAGTGTGTGACCA 275
QY 579 ATGACAAACAACATTAATTAATGAGCATGAGATAGCTGTCAATCAATTAATCA 638
Db 276 ATGACAAACAACATTAATTAATGAGCATGAGATAGCTGTCAATCAATTAATCA 335
QY 639 ACGGTGATTAATTAATTAATCAAGATTAATCACTAAGTT 674


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Db      336  ACCGGATTAAATTATATCAAGATTAACCTTAGTT 371
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RESULT 5  BE804790      409 bp  mRNA  linear  EST 06-DEC-2001
LOCUS      BE804790
DEFINITION  s845f11.y1 Gm-cl061 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl061-1702 5' similar to TR:Q39028 Q39028 ATMYB2. ; mRNA
sequence.
ACCESSION  BE804790
VERSION     BE804790
KEYWORDS    GI:10235902
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 409)
AUTHORS     Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
            This clone is available through: Reggen, Invitrogen Corp. 2130
            South Memorial Parkway Hunttsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@reggen.com
            Insert Length: 1068 Std Error: 0.00.
FEATURES
    source
        1..409
            /organism="Glycine max"
            /db_xref="taxon:3847"
            /clone="GENOME SYSTEMS CLONE ID: Gm-cl061-1702"
            /clone_1lb="Gm-cl061"
            /feature_type="mature flowers of field grown plants"
            /lab_host="DH10B"
            /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
            XhoI; The cDNA library was constructed from mRNA isolated
            from mature flowers of field grown plants for the cultivar
            Raiden. Complementary DNA was synthesized from mRNA using
            a primer consisting of a poly(dT) sequence with a XhoI
            restriction site. EcoRI adapters were ligated to the
            blunt-ended cDNA fragments followed by XhoI digestion. The
            cDNA fragments were directionally cloned into the
            EcoRI-XhoI restriction site of the pBluescript vector. The
            ligated cDNA fragments were transformed into DH10B host
            cells (GibcoBRL). This library was constructed in the
            laboratory of Dr. Randy Shoemaker."
BASE COUNT  136 a      87 c      97 g      89 t
ORIGIN
Query Match      6.5%; Score 56; DB 12; Length 409;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      215  TACCTCGTCTGATGTTAGAGAGGGAATATTACACCCGAGAACACTTTTGAT 270
|||||
Db      220  TACCTCGTCTGATGTTAGAGAGGGAATATTACACCCGAGAACACTTTTGAT 275
|||||
RESULT 6  BM527606
BM527606

```

```

LOCUS      BM527606      501 bp  mRNA  linear  EST 19-FEB-2002
DEFINITION  sal63906.y1 Gm-cl061 glycine max cDNA clone SOYBEAN CLONE ID:
Gm-cl061-3780 5' similar to TR:Q39028 Q39028 ATMYB2. ; mRNA
sequence.
ACCESSION  BM527606
VERSION     BM527606
KEYWORDS    GI:18733434
SOURCE      soybean.
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 501)
AUTHORS     Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
            Public Soybean EST Project
            Unpublished (1999)
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: estewatson.wustl.edu
            This clone is available through: Reggen, Invitrogen Corp. 2130
            South Memorial Parkway Hunttsville, AL 35801 For further information
            call: (800)-533-4363 or contact: ccu@reggen.com web site:
            www.reggen.com
            Seg primer: -40RP from Gibco
            High quality sequence scop: 421.
FEATURES
    source
        1..501
            /organism="Glycine max"
            /db_xref="taxon:3847"
            /clone="SOYBEAN CLONE ID: Gm-cl061-3780"
            /clone_1lb="Gm-cl061"
            /feature_type="mature flowers of field grown plants"
            /lab_host="DH10B"
            /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
            XhoI; The cDNA library was constructed from mRNA isolated
            from mature flowers of field grown plants for the cultivar
            Raiden. Complementary DNA was synthesized from mRNA using
            a primer consisting of a poly(dT) sequence with a XhoI
            restriction site. EcoRI adapters were ligated to the
            blunt-ended cDNA fragments followed by XhoI digestion. The
            cDNA fragments were directionally cloned into the
            EcoRI-XhoI restriction site of the pBluescript vector. The
            ligated cDNA fragments were transformed into DH10B host
            cells (GibcoBRL). This library was constructed in the
            laboratory of Dr. Randy Shoemaker."
BASE COUNT  170 a      104 c      114 g      113 t
ORIGIN
Query Match      6.5%; Score 56; DB 13; Length 501;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      215  TACCTCGTCTGATGTTAGAGAGGGAATATTACACCCGAGAACACTTTTGAT 270
|||||
Db      196  TACCTCGTCTGATGTTAGAGAGGGAATATTACACCCGAGAACACTTTTGAT 251
|||||
RESULT 7  A1930997      523 bp  mRNA  linear  EST 30-NOV-2001
LOCUS      A1930997
DEFINITION  s845h07.y1 Gm-cl015 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl015-278 5' similar to TR:Q39028 Q39028 ATMYB2. ; mRNA
sequence.

```


ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISMA1930997
A1930997.1 GI:5666961
EST.
soybean.
Glycine maxREFERENCE
AUTHORSEukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 523)TITLE
JOURNAL
COMMENTShoemaker, R., Kaim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gldco
High quality sequence stop: 422.
Location/QualifiersFEATURES
source1..523
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-278"
/clone_id="Gm-c1015"
/tissue_type="Mature flowers, field grown plants"
/lab_host="XLI0-Gold"
/note="Vector: pBluescript II XR, Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI0-gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."BASE COUNT
ORIGIN

172 a 124 c 111 g 115 t 1 others

Query Match 6.5%; Score 56; DB 9; Length 523;
Best Local Similarity 100.0%; Pred. No. 7e-05;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 TACCTCCGTCCTGATGTTAGAGGAGATATTACACCCGAGGAACAATTGGAT 270
Db 244 TACCTCCGTCCTGATGTTAGAGGAGATATTACACCCGAGGAACAATTGGAT 299RESULT 8
LOCUS
DEFINITIONBM527774 552 bp mRNA linear EST 19-FEB-2002
sal65903.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1061-4134 5' similar to TRIO49020 O49020 MYB-LIKE DNA-BINDING DOMAIN PROTEIN.; mRNA sequence.ACCESSION
VERSION
KEYWORDSBM527774 GI:18733722
EST.SOURCE
ORGANISMsoybean.
Glycine maxREFERENCE
AUTHORSEukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 552)
Shoemaker, R., Kaim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marr, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com
Seq primer: -40RP from Gldco
High quality sequence stop: 426.
Location/QualifiersFEATURES
source1..552
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4134"
/clone_id="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="BDH10B"
/note="Vector: pBluescript II SK+, Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GldcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."BASE COUNT
ORIGIN

184 a 118 c 111 g 139 t

Query Match 6.5%; Score 56; DB 13; Length 552;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;Qy 215 TACCTCCGTCCTGATGTTAGAGGAGATATTACACCCGAGGAACAATTGGAT 270
Db 43 TACCTCCGTCCTGATGTTAGAGGAGATATTACACCCGAGGAACAATTGGAT 98RESULT 9
LOCUS
DEFINITION
ACCESSION
KEYWORDS
ORGANISMBE658316 782 bp mRNA linear EST 24-MAY-2001
GM700005B10E4 Gm-r1070 Glycine max cDNA clone Gm-r1070-1759 3', mRNA sequence.BE658316 GI:9984208
EST.
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

REFERENCE 1 (bases 1 to 782)
 Glycine.
 Vodka, L., Kelm, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V.,
 Expelding, U., Rapp, C., Shoop, E., Pardinas, J., Liu, L., and Lewin, H.
 A Functional Genomics Program for Soybean (NSF 9872565)
 Unpublished (1999)
 TITLE Other ESTs: A1930997 corresponding to Gm-c1015-278 (5')
 JOURNAL Contact: Vodka, L.O., PI, A Functional Genomics Program for
 COMMENT Soybean (NSF 9872565)
 Lewin, H. A., Director, Keck Center for Comparative and Functional
 Genomics
 University of Illinois
 Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
 Tel: (217) 244-6147
 Fax: (217) 333-4582
 Email: l.vodka@uiuc.edu
 This clone is available through: Genome Systems, Inc. 4633 World
 Parkway Circle St. Louis, Missouri 63134. For further information
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)
 427-3324 or contact: clones@genomesystems.com or info@genome
 systems.com web site: www.genomesystems.com
 Seq primer: 5'-TTTTTTTTTTTTTTTTTTT(A/C/G)-3'
 Location/Qualifiers
 1. 782
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="Gm-r1070-1759"
 /clone_1lb="Gm-r1070"
 /note="The library Gm-r1070 is a sequence-driven, rerecked
 set of 9,216 clones selected from cDNA libraries from
 various tissues and stages of development of soybean that
 represent 2,639 sequences from immature cotyledons, 1,770
 from immature seed coats, 3,938 from flowers, and 869
 from young pods. The 5' ESTs of the source clones from
 the different libraries was used to select singletons, or
 a representative of each contig, which were rerecked to
 form library Gm-r1070. The cDNA clones of the rerecked
 Gm-r1070 library were then sequenced at the 3' end. The
 contig analysis to select unique genes was performed by
 the laboratory of Ernest Retzel, Center for Computational
 Genomics and Bioinformatics, University of Minnesota,
 http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
 . Rerecking was performed by Genome Systems, St. Louis,
 http://www.genomesystems.com, and 3' sequencing by the
 Keck Center for Comparative and Functional Genomics,
 University of Illinois,
 http://www.life.uiuc.edu/biotech/keck.html. Note: The
 corresponding 5' EST from each clone in the Gm-r1070
 library is listed in the 'OTHER EST' field. The detailed
 information on the source library for each clone can also
 be obtained by referring to the Genome Systems clone ID of
 the original cDNA library that is also listed under
 'OTHER EST'."

BASE COUNT 215 a 144 c 143 g 253 t 27 others
 ORIGIN
 Query Match 5.8%; Score 50; DB 10; Length 782;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 CACGCAAACTGGGAAACAGTGTCTCAAAATTGCCAGCATCTACCTGG 330
 |||||
 Db 612 CACGCAAACTGGGAAACAGTGTCTCAAAATTGCCAGCATCTACCTGG 563

RESULT 10
 AM432229 213 bp mRNA linear EST 03-DEC-2001
 LOCUS bh70908.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
 DEFINITION Gm-c1015-5175 5', mRNA sequence.
 ACCESSION AM432229
 VERSION AM432229.1 GI:6963536
 KEYWORDS EST.

SOURCE
 ORGANISM soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 213)
 REFERENCE Shoemaker, R., Kelm, P., Vodka, L., Expelding, U., Corryell, V., Khanna
 AUTHORS A., Bolle, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
 R., Ratter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
 R., Waterston, R., and Wilson, R.
 Public Soybean EST Project
 Unpublished (1999)
 TITLE Public Soybean EST Project
 JOURNAL Contact: Shoemaker R/ Public Soybean EST Project
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: ccu@resgen.com
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1. 213
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5175"
 /clone_1lb="Gm-c1015"
 /tissue_type="Mature flowers, field grown plants"
 /lab_host="X110-Gold"
 /note="Vector: pBluescript II XR; Site 1: EcoRI, Site 2:
 XhoI. This cDNA library was constructed from mRNA isolated
 from mature flowers of field grown plants. The cDNA
 library was prepared using the Stratagene pBluescript II
 XR cDNA library construction kit. Complementary DNA was
 synthesized from mRNA using a primer consisting of a poly
 (dT) sequence with a XhoI restriction site. EcoRI adapters
 were ligated to the blunt-ended cDNA fragments followed by
 XhoI digestion. The cDNA fragments were directionally
 cloned into the EcoRI-XhoI restriction site of the
 pBluescript vector. The ligated cDNA fragments were
 transformed into X110-Gold host cells. This library was
 constructed by Dr. Randy Shoemaker and Dr. John
 Expelding."

BASE COUNT 69 a 47 c 36 g 61 t
 ORIGIN
 Query Match 5.7%; Score 49; DB 10; Length 213;
 Best Local Similarity 100.0%; Pred. No. 0.0075;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 ACAATTATCTCTGATCAATCTCACTGTGTGACCAATGACAACAACAACA 593
 |||||
 Db 84 ACAATTATCTCTGATCAATCTCACTGTGTGACCAATGACAACAACAACA 132

RESULT 11
 BG652172/c 516 bp mRNA linear EST 29-NOV-2001
 LOCUS bad75b05.y1 Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE
 DEFINITION ID: Gm-c1051-5842 5' similar to TR:Q9SBG4 Q9SBG4 PUTATIVE
 TRANSCRIPTION FACTOR ;, mRNA sequence.
 ACCESSION BG652172
 VERSION BG652172.1 GI:13789581
 KEYWORDS EST.
 ORGANISM soybean.
 Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 516)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

TITLE
JOURNAL

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Possible reversed clone: similarity on wrong strand. This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway, Huntsville, AL 35801. For further information call: (800) 533-4363 or contact via email: ccu@resgen.com

FEATURES

High quality sequence stop: 310.

Location/Qualifiers

1..516

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-5842"

/clone_1lb="Gm-c1051"

/tissue_type="floral meristematic mRNA"

/lab_host="DH10B"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from floral meristematic mRNA provided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT
ORIGIN

162 a 78 c 89 g 187 t

Query Match

Best Local Similarity 100.0%; Score 49; DB 12; Length 516;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 ACAATTATCCTGATCAATCCAGTTGTTGACCAATGACAACAACA 593

DB 396 ACAATTATCCTGATCAATCCAGTTGTTGACCAATGACAACAACA 348

RESULT 12

BM732162/c

LOCUS

DEFINITION

BM732162

VERSION

KEYWORDS

SOURCE

ORGANISM

soybean.

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 567)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

REFERENCE
AUTHORS

Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway, Huntsville, AL 35801. For further information call: (800) 533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gldco

High quality sequence stop: 422.

Location/Qualifiers

1..567

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="SOYBAN CLONE ID: Gm-c1061-4914"

/clone_1lb="Gm-c1061"

/tissue_type="mature flowers of field grown plants"

/lab_host="DH10B"

/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Ralden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT
ORIGIN

175 a 88 c 101 g 203 t

Query Match

Best Local Similarity 100.0%; Score 49; DB 14; Length 567;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 545 ACAATTATCCTGATCAATCCAGTTGTTGACCAATGACAACAACA 593

DB 387 ACAATTATCCTGATCAATCCAGTTGTTGACCAATGACAACAACA 339

RESULT 13

BE805071

LOCUS

DEFINITION

BE805071

VERSION

KEYWORDS

SOURCE

ORGANISM

soybean.

Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 395)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,

Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann

TITLE
JOURNAL
COMMENT

R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cdu@resgen.com
High quality sequence stop: 367.

FEATURES

source

location/Qualifiers

1..395

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1061-877"

/clone_1lb="Gm-c1061"

/tissue_type="mature flowers of field grown plants"

/lab_host="DH10B"

/note="Vector: pBluescript II SK+, Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT

127 a 86 c 103 g 79 t

Query Match

Best Local Similarity 5.4%; Score 47; DB 12; Length 395;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 TACTCCGTCCTGATGTTAGAGAGGAAATATTACACCGAGAAC 261

Db 195 TACTCCGTCCTGATGTTAGAGAGGAAATATTACACCGAGAAC 241

RESULT 14
AM423958 425 bp mRNA linear EST 03-DEC-2001
LOCUS
DEFINITION
AM423958.1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1015-3993 5' similar to TR:Q49020 O49020 MYB-LIKE DNA-BINDING DOMAIN PROTEIN.; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS
1 (bases 1 to 425)
Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

FEATURES

source

location/Qualifiers

1..425

/organism="Glycine max"

/db_xref="taxon:3847"

/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-3993"

/clone_1lb="Gm-c1015"

/tissue_type="mature flowers, field grown plants"

/lab_host="XL10-Gold"

/note="Vector: pBluescript II SK+, Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II SK+ cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelidg."

BASE COUNT

130 a 95 c 107 g 93 t

Query Match

Best Local Similarity 5.4%; Score 47; DB 10; Length 425;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 TACTCCGTCCTGATGTTAGAGAGGAAATATTACACCGAGAAC 261

Db 160 TACTCCGTCCTGATGTTAGAGAGGAAATATTACACCGAGAAC 206

RESULT 15
BE807621 467 bp mRNA linear EST 06-DEC-2001
LOCUS
DEFINITION
BE807621.1 Gm-c1061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1061-33 5' similar to TR:Q39028 Q39028 ATMYB2.; mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE
AUTHORS
1 (bases 1 to 467)
Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available through: ResGen, Invitrogen Corp. 2130
 South Memorial Parkway Huntsville, AL 35801 For further information
 call: (800)-533-4363 or contact via email: cu@resgen.com
 Insert length: 1403 Std Error: 0.00
 High quality sequence stop: 411.

FEATURES

Source:

1. .467
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1061-33"
 /clone_id="Gm-c1061"
 /tissue_type="mature flowers of field grown plants"
 /lab_host="DH10B"
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 from mature flowers of field grown plants for the cultivar
 Ralston. Complementary DNA was synthesized from mRNA using
 a primer consisting of a poly(dT) sequence with a XhoI
 restriction site. EcoRI adapters were ligated to the
 blunt-ended cDNA fragments followed by XhoI digestion. The
 cDNA fragments were directionally cloned into the
 EcoRI-XhoI restriction site of the pBluescript vector. The
 ligated cDNA fragments were transformed into DH10B host
 cells (GibcoBRL). This library was constructed in the
 laboratory of Dr. Randy Shoemaker."

BASE COUNT 154 a 78 c 105 g 130 t
 ORIGIN

Query Match

Best Local Similarity 5.4%; Score 47; DB 12; Length 467;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 215 TACCTCCGCTGATGTTAGAGAGGAATATTACCCGAGGACA 261
 ||||||||||||||||||||||||||||||||||||||||
 Db 177 TACCTCCGCTGATGTTAGAGAGGAATATTACCCGAGGACA 223

Search completed: February 8, 2003, 11:07:15
 Job time : 2058 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: February 8, 2003, 10:33:30 ; Search time 2673 Seconds

(without alignments)
2242.865 Million cell updates/sec

Title: US-10-021-811-36

Perfect score: 1138

Sequence: 1 MDKQCKTSQDEVRKGPW.....NNINYSMEDSMQULNGD 206

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODL=frame+ p2n.model -DEV=xlh
-O=/cgm2_1/USPTO.epool/US10021811/runat.03022003.111222.25637/app.query.fasta_1.391
-DB=genmb1 -QFMT=laetap -SOFIX=eye -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=Dlosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptco -NORM=ext -HEAPSIZE=570 -MINLEN=0 -MAXLEN=200000000
-USER=US10021811 @CGN 1.1 2425 @runat.03022003.111222.25637 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAR -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WAO TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hc:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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10: gb_ro:*
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12: gb_ey:*
13: gb_un:*
14: gb_vt:*
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16: em_fun:*
17: em_hum:*
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19: em_mu:*
20: em_cm:*
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23: em_pat:*
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26: em_ro:*
27: em_sbs:*
28: em_un:*

29: em_vt:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_ey:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	909.5	79.9	1022	8	PSMYB26	Y1105 P. sativum m
2	671	59.0	910	8	AY086615	AY086615 Arabidops
3	667	58.6	645	8	AF175987	AF175987 Arabidops
4	653.5	57.4	1033	8	AB005888	AB005888 Arabidops
5	585	51.4	1127	8	AY088761	AY088761 Arabidops
6	570	50.1	872	8	AB058642	AB058642 Lilium hy
7	520	45.7	1295	8	CPJ31917	U33917 Craterostig
8	519.5	45.7	105543	8	ATKCO09325	AC009325 Arabidops
9	518	45.5	1343	8	AY026332	AY026332 Oryza sat
10	515.5	45.3	1117	8	AF510112	AF510112 Craterost
11	514.5	45.2	133242	8	AP003140	AP003140 Oryza sat
12	514.5	45.2	145491	8	AP002883	AP002883 Oryza sat
13	510	44.8	1423	8	AF262733	AF262733 Arabidops
14	497	43.7	1140	8	AF334815	AF334815 Arabidops
15	485	42.6	931	8	AY008377	AY008377 Arabidops
16	479	42.1	853	8	AF474132	AF474132 Sorghum b
17	476.5	41.9	126599	2	AP003816	AP003816 Oryza sat
18	464	40.8	817	8	AY133705	AY133705 Arabidops
19	461.5	40.6	1033	8	AF034133	AC016447 Arabidops
20	458	40.2	107816	8	AC016447	U62743 Arabidops
21	453.5	39.9	1070	8	ATU62743	U62743 Arabidops
22	446.5	39.2	158826	8	AP003607	AP003607 Oryza sat
23	446.5	39.2	197674	2	AP004367	AP004367 Oryza sat
24	440	38.7	1262	8	AF371980	AF371980 Arabidops
25	435.5	38.3	1558	8	CPJ31916	U33916 Craterostig
26	427.5	37.6	1024	8	AF062894	AF062894 Arabidops
27	427.5	37.6	114652	2	AC118288	AC118288 Oryza sat
28	426.5	37.5	134673	8	AP002860	AP002860 Oryza sat
29	425.5	37.4	2205	8	AB052240	AB052240 Arabidops
30	422	37.1	197135	2	AC124961	AC124961 Medicago
31	416.5	36.6	2131	8	PHMYBPH33	Z13998 P. hybrida m
32	415.5	36.5	771	8	AF272733	AF272733 Arabidops
33	413.5	36.3	1057	8	PHMYBPH22	Z13997 P. hybrida m
34	413	36.3	1155	8	AY059820	AY059820 Arabidops
35	411.5	36.2	90077	8	AP004915	AP004915 Lotus jap
36	410	36.0	960	8	AF175991	AF175991 Arabidops
37	410	36.0	1032	8	AY081512	AY081512 Arabidops
38	408	35.9	2220	8	AB052242	AB052242 Arabidops
39	408	35.9	2222	8	AB052245	AB052245 Arabidops
40	407	35.8	967	8	ATWYBRTF	Z68158 A. thaliana
41	406.5	35.7	1132	8	AY096523	AY096523 Arabidops
42	406.5	35.7	1512	8	AY063939	AY063939 Arabidops
43	405	35.6	2221	8	AB052244	AB052244 Arabidops
44	405	35.6	2221	8	AB052249	AB052249 Arabidops
45	404	35.5	795	8	AB029160	AB029160 Glycine m

RESULT 1

ALIGNMENTS

PSMYB26	PSMYB26	1022 bp	mRNA	linear	PLN 09-FEB-1998
LOCUS					
DEFINITION	P. sativum mRNA for Myb-like protein (Myb26).				
ACCESSION	U11105				
VERSION	U11105.1	GI:1841474			
KEYWORDS	Myb-like protein; Myb26.				
SOURCE	Plum sativum.				
ORGANISM	Plum sativum.				

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

2 (bases 1 to 1022)
Strommer,J.N.
Direct Submission
Submitted (05-FEB-1997) J.N. Strommer, University Of Guelph,
Molecular Biology And Genetics, Guelph, Ontario N1G 2W1, CANADA
Location/Qualifiers
1..1022

US-10-021-811-36 (1-206) x PSMYB26 (1-1022)

QY	1	MeLAspLYsVlySGInGInCYeLYeThSeGcIAspProG1vAlAArgYsG1YProTrp	20
QY	2	25
Db	92	ATGGCAAAAAA---CCCTGCACCTCATCTCCAGATCTCGAAGTGAAGAAAGGGCCATCG	145
QY	21	ThrMeGInGInLAspLeuIIELeuMeAsnTYrIIAlAsAsnHISG1GInG1YvAlTrp	40
QY	149	ACCATGGAAGAAAGACTTATATTTTATGATCAATTATATTTGCAAAATCATATGAGAGTCTTGG	205
Db	41	AsnSerLeuAlAlyAlAlAG1YLeuLYaArgAmG1YLYSeCYaArgLeuArgTrp	60
QY	209	AATTCCTTAGCCAAAGCGTCGCTGCTTAAACGACGCGAAAGATTCACAGGCTTCGATGG	265
Db	61	LeuAsnTYrLEuAspRProAspVAlAArgArgLYAsnIIEThProGInGInGInLeuLeu	80
QY	269	TAAACATCTCTTCGCGCGAGTGTAAAGAGGAAATATATACCTCGAGAGAAACAATTGG	325
Db	81	ILMeTG1uLcunHISAlAlyeTTPRG1YAsnArgTTPSerLYeISAlAlAlyeHISLeuPro	100
QY	329	ATCATGCAACTTCATCAAAATGGCGAAATAGGTGATCCAAAATTTGGCAAAACCATCTTCCA	385
Db	101	G1YArgThrAspAsnGInuILEuAsenTYrTTPArgThrArgILEGInLYeHISILEuYS	120

Db	389	GGAGAACTGACAAAGAGATTAGGAATTTTGGAGCATAGAGATCAAAAGCACACTTAG	448
Qy	121	GINALA-----GluAsnProGlnGlnSerSerAsnAsnSerGluLe	135
Db	449	CAAGTTGATTAACCTTAATCAACAATTTTTCAGCAAAATGAGG-----TTAGAGATA	502
Qy	136	AsnAsp-----HisGlnAlaSerThrSerHisValSerThreCala	149
Db	503	ATAGATCATCAACCATCATCATCTTATCAACCAAGATGATTAACCAAGTTCTTAATTTGGTA	562
Qy	150	GluProMetGluMetTyrSerProProCysTyrGlnGluMetLeuGluProPheSerThr	169
Db	563	GAGCCAAATGGAAACTTATTCTCCAACTTCATATCAAGAACTTTGGAGCCATTTCCAACT	622
Qy	170	GlnPheProThrIleAsnProAsp-----GlnSerSerCysCysThrAsnAsn	186
Db	623	CAATTTCCACGATTAATTAATGATCATCATCAAAACTCAATTTGTTGGCCAAATGACAC	682
Qy	187	AsnAsnIleLeuTyrTyrPheMetGluAspSerTyrPheMetGlnLeuLeuAsnGlyAsp	206
Db	683	ATAATCAACAATTAATTTGAGCATGAGGATATTCGGTCAATGACATTAATCAATGAGGAT	742

LOCUS	AY086615	910 bp	mRNA	linear	PLN 25-JUN-2002
DEFINITION	Arabidopsis thaliana clone 262460	mRNA, complete sequence.			
ACCESSION	AY086615				
VERSION	AY086615.1	GI:21405325			
KEYWORDS	PL1 CDNA.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				

COMMENT

This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unsplined introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laet ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genest carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

SOURCE

CDs	110. 754	/codon_start=1	/product="putative transcription factor MYB24"
		/protein_id="AA63674.1"	
		/db_xref="GI:21554734"	
		/translation="MEKRSSSGGSGGDAEVRKGPWTEEDLILINVAHKGKGVNS LASAGLARTGKSCRLWNLVRLPDVYRNGTPEEOLITIELAKGNRWSLAKLHP GRNDIEKNFMRTIOKYIIKSGEITTVGSOSSEFINHAHTSHVNDVDETMDYSP TTSYQHASNINQOLATNGYINRYPSVDSIMPLSDQSBQNTWSYVDLPMNINYN"	
BASE COUNT	307 a 169 c 185 g 249 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1,13e-60	Length:	910
Score:	671.00	Matches:	133
Percent Similarity:	72.90%	Conservative:	23
Best Local Similarity:	62.15%	Mismatch:	50
Query Match:	58.96%	Indels:	8
Db:	8	Gaps:	4
US-10-021-811-36 (1-206) x AY066615 (1-910)			
Qy	1 MetApLybLySgInGInCys-----LysThrSerGInaPProGInuValArgLySeGly	18	
Db	110 ATGGAGAAAGAGAAAGAGTAGTGTTCTCGATCAGAGATGACAGAGTAGAGAAAGG	169	
Qy	19 ProTPRTHMetGInGInaSPLeuLeuMetAenTYrIleAlaAsnHISglYgInGly	38	
Db	170 CCATGACGATGAGAGAAAGATTGATTCTCATCATATTATGCGCAATCATGTGAAAGT	229	
Qy	39 ValTPaenSerLeuAlaAlaGlyLeuLYbaTgaenGlyLySerCyArGLeu	58	
Db	230 GTTTGGAATCTCTCGCCAAATCTCAGAGACTAAACGACCGGAGAAAGTTGCGGCTC	289	
Qy	59 ArgTPLeuAsnTYrLeuArProAspValArgaTgGlyAsnHISLeThProGInGIn	78	
Db	290 CGGTGCTGACTTACCTCGACCTGATGCGACGGGAGAAATATCACACACAGAAACAG	349	
Qy	79 LeuLeuLeMetGInuLeuHISAlaLYSTpGlyAsnArgTTPSerLySleAlaLySHIS	98	
Db	350 CTCACCATCATGAACTTCATCAAAATGGGAAATAGGTGTCAAAAATTGCAAGCAT	409	
Qy	99 LeuProGInArgThAspAsnGInuLeLYsaenTYrTPArgThArgLISgInLySHIS	118	
Db	410 TTACACAGAGAGACGACATAGATAAAGAACTTTGGAGGACTAGATCCAGAAATTC	469	
Qy	119 IleLYSgInAlaGInuAsnPhGInGInGInSerSerAsnAsnSerGInuLeaAsnPHIS	138	
Db	470 ATCATCAAGCGCGAGAAACAGACCGCTGTATCAAAAGCTTCGAGTTATTAACAT	529	
Qy	139 GInAlaSerThSerHISVal---SerThMetAlaGInuProMetGInuMetYrSerPro	157	
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Qy	158 ProCYrTYGInGInLYMetLeuGInuProPheSerThGInPhProThrIleAsn-----	175	
Db	590 ACGAGCTCGTATCACATGCGACGAATATTATACAGACGCTTAATTATGTAATTATGCG	649	
Qy	176 ProAspGInSerSerCYs-----CYrThAsnAspAsnAsnHISleAsnTYrTP	192	
Db	650 CCGTAATCCAGTTCCATCATGATGATGATGATGATGATGATGATGATGATGATGATG	709	
Qy	193 SerMetGInaSPSerThSerMetGInuLeuAsnGInaSP	206	
Db	710 AGGTGATGATCTTTGGCCCATGAAATATATATATATATATATATATATATATAT	751	
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LOCUS	AF175987		PLN 30-AUG-2002
DEFINITION	Arabidopsis thaliana putative transcription factor (MYB24) mRNA,		
ACCESSION	AF175987		
VERSION	AF175987.1	GI:5823306	

	KEYWORDS	Arabidopsis thaliana.
SOURCE	SOURCE	Arabidopsis thaliana
ORGANISM	ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Equisetopsida; Magnoliopsida; eudicotyledons; core eudicots; Rosidae; eurosoids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE	REFERENCE	1 (bases 1 to 645)
AUTHORS	AUTHORS	Kranz,H.D., Denekamp,M., Grew,R., Jin,H., Leyva,A., Meisner,R.C., Petroni,K., Urrutiqui,A., Beyer,N., Martin,C., Smeekens,S., Tonelli,C., Paz-Ares,J. and Weishaar,B.
TITLE	TITLE	Towards functional characterisation of the members of the R2R3-MYB gene family from Arabidopsis thaliana
JOURNAL	JOURNAL	Plant J. 16 (2), 263-276 (1998)
MEDLINE	MEDLINE	99056848
PUBMED	PUBMED	9839469
REFERENCE	REFERENCE	2 (bases 1 to 645)
AUTHORS	AUTHORS	Stracke,R., Weider,M. and Weishaar,B.
TITLE	TITLE	The R2R3-MYB gene family in Arabidopsis thaliana
JOURNAL	JOURNAL	Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
MEDLINE	MEDLINE	21481677
PUBMED	PUBMED	11597504
REFERENCE	REFERENCE	3 (bases 1 to 645)
AUTHORS	AUTHORS	Stracke,R. and Weishaar,B.
TITLE	TITLE	Direct Submission
JOURNAL	JOURNAL	Submitted (06-AUG-1999) Dept. Biochemie, Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
FEATURES	FEATURES	Location/Qualifiers
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CDS	CDS	1..645
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BASE COUNT	BASE COUNT	219 a 125 c 153 g 148 t
ORIGIN	ORIGIN	
Alignment Scores:	Alignment Scores:	
Pred. No.:	Pred. No.:	1.95e-60 Length: 645
Score:	Score:	667.00 Matches: 132
Percent Similarity:	Percent Similarity:	72.43% Conservative: 23
Best Local Similarity:	Best Local Similarity:	61.68% Mismatches: 51
Query Match:	Query Match:	58.61% Indels: 8
DB:	DB:	Gaps: 4
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Dd	Dd	1 ATCGACAAAAGAAGAAATGATGGTGCGGTCTGGATCAGAGATGCACAGGTGAGAAAGGG 60
Qy	Qy	19 ProTrpThMeGlUglUnApLeuIlleUmeCaenTyrlleaIsahniEgLyglUgly 38
Dd	Dd	61 CCATGACCATGGAAGAAATTGATTTCATCAATTAATGCGCCATCATGTGAAGGT 120
Qy	Qy	39 ValTPAsnSerIeuAlalyslaaglyLeuLySaGaanglyLVysSerCyARgLen 58
Dd	Dd	121 GTTTGAACCTCTCGCAAATCTGCAGAGACTAAACGCCAGCGGAAAAAGTTGCCGGCTC 180
Qy	Qy	59 ArgTrpLeuasnTyrlEuArProAspValaRGAYGGLYAAnllEtHrProGluIngn 78
Dd	Dd	181 CGGTGGCTAAACTCCGACCCTGATGTGGCAGCGGGGAAATATACACCAAGAACACG 240

AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
TITLE Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1127)
AUTHORS Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or later ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genes carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

FEATURES

source

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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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Pred. No.: 1,35e-51 Length: 1127
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Best Local Similarity: 55.50% Mismatches: 44
Query Match: 51.41% Indels: 32
DB: Gaps: 6

US-10-021-811-36 (1-206) x AY088761 (1-1127)

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OY 15 ValAarglybglProtrpThmetGlnuaspLeuileuMetAasnyrIlealaasn 34
DB 346 GTGAAGAAAGAGCTTGGACTTGTGAGAAAGATTTCATCTCTTAATTAATCTTAAAT 405
OY 35 HisgljgluglYvalTtpAsnSerleuAlalyaAlaaglyLeuLyAaRnglyY 54
DB 406 CATGTGGAAGGCTTTGGAACTCTGTCCGCAAAAGCTCGGTCTAAACGTAACGAAAA 465
OY 55 SerCyAaRgluAaRgTtpLeuAasnyrTleuAaRgProaapValaAaRgLyAa 74
DB 466 AGTTGTGGCTCGGTGGTGAACATATCTCCACAGATGTGGCGGAGGAAACATAAC 525
OY 75 ProgluglGlnLeuLeuileuMetGlnuaspLeuAlalySTripGlyAaAaRgT 94
DB 526 ACAGAAAGAAAGCTTTGATCATCTCACTTCACTTAAGCTTGAAGAAAGGTGTG 585

OY 95 IleAlalyHisleuProglYArGrThraspaRngulileYAsenTYrTpaRgThra 114
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OY 115 IleglnlyHisIlelyeGlnAlaGlu-----AaspheGlnGlnSerSer 130
DB 646 ATTCAGAGACATGAAAGTGCATCGGAAATAATGATGAATCATCAATCATTTTCG 705
OY 131 AaspAsnSerGlnleAaA-----AphiSglnAlaSerThrSerHisValSerThrMet 148
DB 706 GGAACATCAAGAGCTCCGGAGATGACAGACGACAGACAGCTCCGCAAGACATAGACAG 765
OY 149 AlaGluProMetGlnMetlySerProProCySTyTrGlnGlyMetleuGlnPropheser 168
DB 766 GCTGAGAGCTTCTCT-----CAGCGAAGACG 792
OY 169 ThrGlnPheProThrIleAsnProaaspGlnSerSerCySThrAaAaAaAaAa 188
DB 793 ACAGCTTTAATGTGTG-----GAACACAGTCAAAAC 825
OY 189 IleAsnTYrTtpSerMetGlnuAaSerTtpSerMetGlnLeuAaAaNGlyAa 206
DB 826 GAGATTAATCGAAGCTTGAGATCTGTGCGCCGTCCACTTCTTAATGTGAC 879

RESULT 6
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DEFINITION AB058642
ACCESSION AB058642.1 GI:13537529
VERSION
KEYWORDS
SOURCE
ORGANISM

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Lilium hybrid division I
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
Lilium; Lilium hybrid cultivars.

REFERENCE
AUTHORS Nakatsuka, A., Izumi, Y. and Yamagishi, M.
TITLE Isolation and characterization of the genes related to anthocyanin biosynthesis in Asiatic hybrid lily
JOURNAL Unpublished

2 (bases 1 to 872)
AUTHORS Nakatsuka, A., Izumi, Y. and Yamagishi, M.
TITLE Direct Submission
JOURNAL Submitted (24-MAR-2001) Akira Nakatsuka, Shimane University, Faculty of Life and Environmental Sciences, Matsikawatsu 1060, Matsue, Shimane 690-8504, Japan
(E-mail:nakatsuka@life.shimane-u.ac.jp, Tel:81-852-32-6502)
FEATURES
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BASE COUNT 269 a 177 c 213 g 213 t
ORIGIN

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Pred. No.: 3.65e-50 Length: 872
Score: 570.00 Matches: 118
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Best Local Similarity: 56.19% Mismatches: 39

Query Match: 50.09% Indels: 36
 DB: 8 Gaps: 5
 US-10-021-811-36 (1-206) x AB058642 (1-872)

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DB 134 ACATGAGAAAGAGATCTCATCTCTCATCATCATGACCAACATGAGGAGGAGATCTGG 193
QY 41 LnsSerLysAlaLysAlaLysLysLysLysLysLysLysLysLysLysLysLysLys 60
DB 194 AACAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 253
QY 61 LeuAerTyrLeuAerProAerPleuValArgArgLysLysLysLysLysLysLysLys 80
DB 254 CTGAATTAACCTGAGGCTGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 313
QY 81 LMetGluLysAlaLysLysLysLysLysLysLysLysLysLysLysLysLysLys 100
DB 314 ATCATGAGAACTTCAACAGACATGGGGTAAACATGATGTCGAAATTCGAAAGAGCTCCA 373
QY 101 GlyArgThrAerAerGluLysLysLysLysLysLysLysLysLysLysLysLysLys 120
DB 374 GAGAGAACAGAAAGAAATCAAGAACTTCAAGAGACCAAGTCCAGAAAG----- 424
QY 121 GlnAlaGluAerPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
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QY 141 SerThrSerHisValSerThrMetAlaGluProMetGlu----- 153
DB 461 TCCATCTCTTGGATGAAACTGATGTCATGCAAGATGCAAGATGTCATGTCGTCGTCG 520
QY 154 -----MetTyrSerProProCysTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 171
DB 521 CAGACGACCTGACATCAAGGCGACGACCTTCAACAACTTGAACGATTTGAAATCTCTTC 580
QY 172 ProThrIleAerProAerGlnSerSerCysCysThrAerAerAerAerAerAerTyr 191
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QY 192 TrpSerMetGluAerSerTrpSerMetGln 201
DB 599 CTGTCCTGCGAGAACTGGGCTATGAG 628

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RESULT 7
 CPU33917
 LOCUS 1295 bp mRNA linear PLN 17-APR-2001
 DEFINITION Craterostigma plantagineum myb-related transcription factor (cpm7)
 mRNA, complete cds.
 U33917
 VERSION U33917.1 GI:1002799
 SOURCE
 ORGANISM
 Craterostigma plantagineum.
 Craterostigma plantagineum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Lamiales; Lamiales incertae sedis;
 Toraleae; Craterostigma.
 1 (bases 1 to 1295)
 Iturriaga, G., Leyna, L., Villegas, A., Gharalbeh, R., Salami, F. and
 Barrios, D.
 A family of novel myb-related genes from the resurrection plant
 Craterostigma plantagineum are specifically expressed in callus and
 roots in response to ABA or desiccation
 Journal Mol. Biol. 32 (4), 707-716 (1996)
 MEDLINE 97134962
 PUBMED 8980522
 REFERENCE 2 (bases 1 to 1295)

AUTHORS Iturriaga, G.
 TITLE Direct Submission
 JOURNAL Submitted (14-AUG-1995) Gabriel Iturriaga, Plant Molecular Biology,
 Instituto de Biociencia, Av. Universidad #2001, Cuernavaca, MOR
 62210, Mexico

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CDS
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/product="cpm7"

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 F"

BASE COUNT 405 a 286 c 279 g 325 t
 ORIGIN

Alignment Scores:

Pred. No.: 9.6e-45 Length: 1295
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 Percent Similarity: 62.38% Conservative: 27
 Best Local Similarity: 50.00% Mismatches: 31
 Query Match: 45.69% Indels: 46
 DB: 8 Gaps: 5

US-10-021-811-36 (1-206) x CPU33917 (1-1295)

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DB 125 ATGAACCAACAGCAGAGTTGTTAAAGTTTCCAAAGAACAAATTAACAGTGAAGCAGAT 184
QY 16 -----ArgLysGlyProTyrTrpThrMetGluGluAerPleuIleuMet 29
DB 185 GATGATTCCTGGACCTCAAGAAAGAGACCGCTGATGATGAAAGCTTCACTATC 244
QY 30 AenTyrTlleAlaSerHisGlyGluGlyValTrpAerSerLysAlaLysAlaLysLys 49
DB 245 AACTACATCGCTCACCATGAGGAGAGATGGAATCTCTTGGACGTTTCGTCGCTGG 304
QY 50 LysAerAerGlyLysSerCysArgLysArgTrpLysAerTyrLeuAerProAerPleuValArg 69
DB 305 AAACGAACCTGAAAGAGCTGACGATGATGATGATGATGATGATGATGATGATGATG 364
QY 70 ArgLysAerTyrProGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 89
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QY 90 AenAerTyrSerLysLysAlaLysHisLysProGluArgTrpAerAerGluLysLys 109
DB 425 AATAGTGTGTCGAAAGATGGCCCAACATTTGCTGGAAGACAGACATGATGATGAAAGAC 484
QY 110 TyrTrpArgTrpArgLysLysLysLysLysLysLysLysLysLysLysLysLys 129
DB 485 TACTGAGAGAGAGAGGTCCTCAAAACATGCCAAACAGCTA-----AAGTGGAC 532
QY 130 SerAerAerSerGluLysAerPleu----- 137
DB 533 GTCAACAGCAACAGCTTAAGACACCATGAGATCACTTGGATGCCAAGATTGCTGAG 592
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Db	653	TGGCGCTGATCCGCGCATGAAATACAGCCCTTACAGCACTGCCATGGCTGACGAGGATCAC	712						
Oy	161	-----GlnGlyMetLeuGluPro	166						
Db	713	CGTCGTCACTTTATGCTGATGCCA	736						

RESULT 8
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 complete sequence.
 AC009325
 AC009325.8 GI:12408717
 HTG.
 Arabidopsis thaliana.
 Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 105543)
 Lin,X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.,
 Rensing,C.M., Koo,H., Fujii,C.Y., Utechtack,T.R., Barnstead,M.E.,
 Bowman,C.L., White,O., Niernann,W.C. and Fraser,C.M.
 Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence
 Unpublished
 2 (bases 1 to 105543)
 Lin,X. and Kaul,S.
 Direct Submission
 Submitted (16-AUG-1999) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org
 3 (bases 1 to 105543)
 Lin,X.
 Direct Submission
 Submitted (24-JAN-2001) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Jan 24, 2001 this sequence version replaced gi:12280821.
 Address all correspondence to:
 Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr.
 Rockville, MD 20850, USA
 E-mail: xlin@tigr.org
 BAC clone F4P13 is from Arabidopsis chromosome III and is near the
 molecular marker ILRI.
 The orientation of the sequence is from SP6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of three methods: Gene
 prediction programs including GRAIL (available by anonymous ftp
 from arthur.gens.com.ornl.gov), GeneFinder (Phil Green, University of
 Washington), Genscan (Chris Burge,
 http://genomic.stanford.edu/~chris/GENSCAN.htm), and NetPlantGene
 (http://www.cbs.dtu.dk/netgene/cbsnetgene.html), searches of the
 complete sequence against a peptide database and the Arabidopsis
 EST database at TIGR (http://www.tigr.org/tdb/at.html).
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as 'unknown' proteins.
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as 'hypothetical' proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
 http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are
 identified by RepeatMasker (Arian Smit,
 http://ftp.genome.washington.edu/RM/RepeatMasker.html). Regions of
 genomic sequence that are not annotated as genes but have predicted
 exons by GRAIL are annotated as misc features.
 Location/Qualifiers
 1..105543

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misc_feature	complement(6934. .6974) /note="exon predicted by xgrail, quality good"
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AUTHORS Lee, M.-W., Qi, M. and Yang, Y.
TITLE A novel jasmonic acid-inducible rice *myb* gene associates with fungal infection and host cell death
JOURNAL Mol. Plant Microbe Interact. 14 (4), 527-535 (2001)
MEDLINE 21204658
PUBMED 11310740
REFERENCE 2 (bases 1 to 1343)
AUTHORS Lee, M.-W. and Yang, Y.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2001) Plant Pathology, University of Arkansas, 217 Plant Science Bldg., Fayetteville, AR 72701, USA
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/cultivar="Drewn"
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127..984
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BASE COUNT 367 a 298 c 337 g 341 t
ORIGIN
Alignment Scores:
Pred. No.: 1.62e-44 Length: 1343
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QY 34 AasnIeGLyGLuGLyValTrpAsnSerLeuAlaIlyAlaIaGLyLeuIlyAsnArgenGly 53
Db 268 GATCAcAGGCGAGGGCGCGTGGAAcGCAcTGCAGcCGGCGCGGTCTGAAAGAGAGACTGG 327
QY 54 IyVSeTCyArGLeuArGrTrpLeuAsnTrIleuArGrProAspValArGrArgGLyAsnIle 73
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Db 388 ACCGcAGAGAGAGAGCTGCTCATCTCTCGACCTCCACTCCGAGTGGGGcAGACGATGCTC 447
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Db	808	GAGAAAGTAGAACCTCAGAAAGCTGATCACAGAGGTGACATGATGTTTGGTCTACAGAG 867
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ACCESSION	AF510112	
VERSION	AF510112.1	GI:21215201
KEYWORDS	complete cds.	
SOURCE	Craterostigma plantagineum.	
ORGANISM	Craterostigma plantagineum.	
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
AUTHORS	Buxarjota; Villalobos, M.A.; Bartels, D. and Iturrriaga, G.	
TITLE	The Craterostigma plantagineum CpMYB10 gene enhances stress	
JOURNAL	tolerance to Arabidopsis transgenic plants	
REFERENCE	unpublished	
AUTHORS	2 (bases 1 to 1117)	
TITLE	Villalobos, M.A. and Iturrriaga, G.	
JOURNAL	Submitted (07-MAY-2002) Plant Molecular Biology, Institute of	
FEATURES	Biotechnology, Universidad Ave. 2001, Cuernavaca, Mor 62210, Mexico	
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Pred. No.:	2,37e-44	Length: 1117
Score:	515.50	Matches: 103
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Query Match: 45.30% Indels: 25
DB: 8 Gaps: 5
US-10-021-811-36 (1-206) x AF510112 (1-1117)

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Oy 7 (YSLYSTRHSGSLASP---ProGluValArgylsGlyProTTPHThMeGluGluAsp 25
Db 130 (YSLYSTRHSGSLASP---ProGluValArgylsGlyProTTPHThMeGluGluAsp 189
Oy 26 (LUILEUMLCAsnTYTTLLeAlAsnHISglYglYglValTTPAsnSerLeuAlAs 45
Db 190 (TTCACACTCATCACTCATCGCTCCATCCATGCGAGAGAGATGGAATCTCTTGACACT 249
Oy 46 (LAlaAGLYLeuLYAsnArgSngLYsSerCySargLeuAgtTTPLeuAsnTYTLeuArg 65
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Oy 66 (TCoAspValA:GArgGLYAsnILeThProGluGluGluLeuLeuIleMeGluLeuHIS 85
Db 310 (CCGACGTTCCGCGAGAAATATATCACTCGAGAGACAGCTTTCATTCTTGAATCCAT 369
Oy 86 (LAlaYSTTPGLYAsnArgTTPSerLYeLLeAlAsnHISLeuProGLYAsnTYThAspAsn 105
Db 370 (TCACTTGGGCAATAGGTGGTGCAGAGATTCCTCCAACTTTGCTGGAAGAGACGACAAAT 429
Oy 106 (GluLeuLYAsnTYTTPArgThArgGLLeGluHISISLeYSGLnAlaGluAsnPh 125
Db 430 (GAGATAAAGAACTACTGAGAGAAAGGCTCCAAAACATGCCAAACAGCTA----- 480
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Db 481 (---AAGTCCGACGTCACAGCAAGAAAGTTCAAAAGACACCATGAGATACCTTTGATGCCA 537
Oy 139 (-----GlnAlaSerThr-----SerHISValSerThr 147
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Oy 148 (MetLlaGluProMetGluMetLYsSerProProCYsTYTglnGlyMetLeuGlu----- 165
Db 598 (GCCCTCCGCGCTGCTCCGCGCATGAAATACAGCTGCTACAGCGCTGCATGGCTGCAGGC 657
Oy 166 (ProPhSerThrglnPhProThrILeAsnProAspGlnSerSerCYsThrAsnAsp 185
Db 658 (GATCACCGCTCGCTGATTATGCTGATGCCAGATTAACGAGACGACGACGACGCCAC 717
Oy 186 (AsnAsnAsnIle 189
Db 718 (AATTAATTCGATG 729

RESULT 11
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LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
DEFINITION BAC clone:OSUNBa0025P13.
ACCESSION AP003140
VERSION AP003140.2 GI:14164491
KEYWORDS Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
SOURCE clone:OSUNBa0025P13.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC
JOURNAL Published Only in Database (2001)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2001) Takuji Sasaki, National Institute of
Agricobiological Resources, Rice Genome Research Program, Kannondai
```

COMMENT

2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@ab.affrc.go.jp, URL: http://ryp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On May 21, 2001 this sequence version replaced gi:12641874.
Genes were predicted from the integrated results of the following:
(GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor
(October 1998 version)). The genomic sequence was searched against
NCBI NonRedundant Protein database, nr
(ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
RGP. Protein homologies of the coding regions were searched against
NCBI NonRedundant Protein database with BLAST2.0. ESTs represent
the identified cDNA sequences using BLAST2.0 with the
corresponding DDBJ accession no. and RGP clone ID.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with EST homology (covering
almost the entire length of partial sequence) is classified as an
'unknown' protein. A gene predicted with a gene prediction program
is classified as a 'hypothetical' protein.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone. This sequence of OSUNBa0025P13 clone has an overlap with
P0702D12 (DDBJ: AP002820) clone at the position 1 to 1534 of 5' end
and with P0487H02 (DDBJ: AP002883) at the position 84175 to 133242
of 3' end. The sequence of this clone starts at the position
135799 of P0702D12 and ends at the position 49068 of P0487H02.
Detailed information on overlap and assembly quality together with
annotation of this entry is available at
http://ryp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES

source

1. 133242

/organism="Oryza sativa (japonica cultivar-group)"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="1"

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6141..6189)}

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6141..6189)}

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SELDMKRRRLCIADVVAHLSYLHDCSPDVHEDYTKNILLDEPRACISDPGIKI

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10972..11067,11175..11258,11346..11448,11534..11616)

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YNKMSQRMPLIYKLMYQICRALAIHNCVGCHADIRQNLIVNPHHQDKLCPDG

SACVLAIVGEINISYICSRVYRAPBELFGATEKTYTALDVNSACVLAELILGGPVEFGD

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VERBEDNHSANHPHASTRPGREOGGEPENGSPRPPTAGAGPPACPTVPVAPADQ
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Alignment Scores:
Pred. No.: 9 236-42 Length: 133242
Score: 514.50 Matches: 111
Percent Similarity: 56.50% Conservative: 28
Best Local Similarity: 45.12% Mismatches: 40
Query Match: 45.21% Indels: 67
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QY 30 AsnTyrTlleAlaAsnHisGlyGluGlyValTyrPheAsnSerLeuAlaAlaGlyLeu 49
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QY 50 LysArgAsnGlyLysSerCysArgLeuAArgTyrPheAsnTyrLeuArgProAspValArg 69
Db 120245 AGCGGACCGGGAGAGAGCTGCCCTCGGTGCTCACTACCTCGGCCACGCGCC 120304
QY 70 ArgGlyAsnIleThrProGluGluGluLeuLeuIleMetGluLeuHisAlaLysTyrGly 89
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QY 90 AsnArgTyrSerLysIleAlaLysHisIleuPheGlyArgTyrThrAspAsnGluIleLysAsn 109
Db 120365 AACCGCTGTCGAGATCGCGGACGACATCGCGGGAGAGACGACAAACAGATCAAGAAC 120424
QY 110 TyrTyrArgThrArgIleGluLysHisIleLysGlnAlaGluAsnPheGluGlnGlnSer 129
Db 120425 TACTGCGGACCGAGGTGCGAGAGACCGCCACGACGCTC-----GGCTCGCAC 120472
QY 130 SerAsnAsnSerGluIleAsnAsp----- 137
Db 120473 GTCAAATGCGCGGACTTCAAGACGCTCATGAGGACCTCTGATGCGCGGCTCTGTGAG 120532
QY 138 -----HisGlnIleAsnThrSerHisValSerThrMetAlaGluProMetGluMetTyr 155

Db 120533 AGATATCCAGCCGCCGCCCTCG-----TCGAACGCCGCCGCCG----- 120574

QY 156 SerProProCys-----TyrGlnGlyMetLeu-----GluPro 166

Db 120575 ---CCGCCCTGTGCGCCGCCGCCGCTAGTACACAGCGCATGTGTGCATCAGCTGACCCG 120631

QY 167 PheSerThr-----GlnPhePro--- 172

Db 120632 TCACACACAGCTCGAGCATGCGAGGTCGTCTGTCAGCCAGCGGAGAGAGTTCCTCCGTG 120691

QY 173 -----ThrLeaspProAspGlnSer 179

Db 120692 TCAGCAACACACACCTGATGACCATGTGGCCAGCGTCACACCGCGAGATTTGCTCC 120751

QY 180 Ser-----CysCysThrAsnApeAsnAAsnIleAsnTyrTrpSer 193

Db 120752 AGCGAGCATATGCGAGCGGCGGCGCCACAGCAGACCGTTGGATGATGATGACATG 120811

QY 194 MetGluApeSerTrpSer 199

Db 120812 TTCCGAGGAGAGCTGGTCC 120829

RESULT 12

AP002883 145491 bp DNA linear PLN 21-MAR-2002

LOCUS AP002883

DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC clone:P0487H02.

ACCESSION AP002883

VERSION AP002883.2 GI:15623781

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0487H02.

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzae; Oryza.

1

REFERENCE

AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.

TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC clone:P0487H02

JOURNAL Published only in Database (2000)

REFERENCE 2 (bases 1 to 145491)

AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.

TITLE Direct Submission

JOURNAL Submitted (11-OCT-2000) Takuji Sasaki, National Institute of Agricultural Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT On Sep 14, 2001 this sequence version replaced gi:10800078. Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI Nonredundant Protein database, nr (http://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RCP. Protein homologs of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0487H02 clone has an overlap with P0682B08 (DBJ: AP003578) clone at the position 73,961 to 145,491 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.
Location/Qualifiers

source

gene

CDS

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gene
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Best Local Similarity: 45.12% Mismatches: 40
Query Match: 45.21% Indels: 67
DB: 8 Gaps: 9
US-10-021-811-36 (1-206) x AP002883 (1-145491)
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QY 30 AsnIyrIleAlaAsnHisGlyGluGlyValIleAsnSerLeuAlaIleAlaGlyLeu 49
DB 36011 GGGTACGTGCGCGGACACCGCGAGGGGCGGTGAAACAGCTGCGCGGGCGGCGCTG 36070
QY 50 LysArgAsnGlyLysSerCysArgLeuArgTyrPLeuAsnIyrLeuArgProAspValArg 69
DB 36071 AGCGCAGCGGAGAGAGCTGCGCGCTCCGTGCTCACTACCTCGCCCGACGTGCGC 36130
QY 70 ArgGlyAsnIleThrProGluGluGluLeuIleMetGluLeuHisAlaIleAsnTyrGly 89
DB 36131 CGGCGGACTTCAACCCCGAGAGAGAGCTGCTCATCTGAGCTTCACTTCCGGTGGGG 36190
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DB 36191 AACCGTGTGTCAGATGTCGAGACGACATGCGGGAGAGACGACAGATCAAGAAC 36250
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QY 130 SerAsnAsnSerGluIleAsnAsp----- 137
DB 36299 GTCAAATAGCCGCGCAATGTCAGAGACGTCATGAGGACCTTGATCGCGGCTGTCGAG 36358
QY 138 -----HisGlnLaseThrSerHisValSerThrMetAlaGluProMetGluMetYr 155
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QY 156 SerProProCys-----TyrGlnGlyMetLeu-----GluPro 166
DB 36401 ---CCGCGGTGTCGCGCGCGCGCTAGTCACAGCGGATGTGCACTACCTGACCGG 36457
QY 167 PheSerThr-----GlnPhePro----- 172
DB 36458 TCAACCAACGACGTGACGATGACAGGCTGTCTGTCACGACGAGCAGATTCCTCGTGG 36517
QY 173 -----ThrIleAsnProAspGlnSer 179
DB 36518 TCGACGACCAACCACTGATGACATGCGCAGCGTCACACGCGACGCGACAGATGTGTC 36577
QY 180 Ser-----CysCysThrAsnAspAsnAsnIleAsnIyrTrpSer 193
DB 36578 AGCAGCAATGCGGACGCGACGCGACGACGACGACGAGCGTTGGATCATGTATGACATG 36637
QY 194 MetGluAspSerTrpSer 199
DB 36638 TTCAGAGGAGAGCTGCTG 36655
RESULT 13
AF262733 1423 bp mRNA linear PLN 30-AUG-2001
LOCUS AF262733
DEFINITION Arabidopsis thaliana putative transcription factor MYB108 (MYB108)
mRNA, complete cds.

ACCESSION AF262733.2 GI:15375290
 VERSION AF262733.2
 KEYWORDS
 SOURCE
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 Arabidopsis thaliana.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1423)
 Stracke, R., Werber, M. and Weishaar, B.
 Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
 JOURNAL MEDLINE 21481677
 PUBMED 11597504
 REFERENCE 2 (bases 1 to 1423)
 Stracke, R. and Weishaar, B.
 Direct Submission
 Submitted (02-MAY-2000) Biochemie, Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany
 3 (bases 1 to 1423)
 Stracke, R. and Weishaar, B.
 Direct Submission
 Submitted (29-AUG-2001) Dept. Plant Breeding and Yield Physiology,
 Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg
 10, Koeln D-50829, Germany
 Sequence update by submitter
 On Aug 30, 2001 this sequence version replaced gi:8101955.
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 AATTTTGTGAGTSSCTTSSNNQFMNDYNNNGQDFGWSNNDYITPENSVAV
 SPASDLREYSAPENPEYSGQMGNSYPDQNLVSSQLPDYPDYSGLDLDELITAM
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 Db 335 AGACTAAGGTGTTAAATCATCTCCGCGCTGACGTCGCGCGGAAACATTACACTTGA 394
 QY 77 GlnGluLeuLeuLleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAla 96
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 QY 97 LysHisLeuProGlyArgThrAspAsnGluLysAsnTrpArgTrpArgIleGln 116
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 QY 133 -----SerGluLeuAsnAspHisGlnAlaSerThrSerHis 144
 Db 575 TACTTGATGATGCTGCTGACTGAGAGAGATTGATGAGCTGCGCTCATTCGCGACA 634
 QY 145 ValSerThrMetAlaGluProMetGluMetLysSerProProCysTrpGlnGlyMetLeu 164
 Db 635 GCAGCCACACAC----- 646
 QY 165 GluProPheSerThrGlnPheProThrIleAsnProAapGlnSerSerCysThrAsn 184
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 AF334815
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 DEFINITION complete cds.
 ACCESSION AF334815
 VERSION AF334815.2 GI:15375294
 KEYWORDS
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 ORGANISM
 Arabidopsis thaliana.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 1140)
 Stracke, R., Werber, M. and Weishaar, B.
 Curr. Opin. Plant Biol. 4 (5), 447-456 (2001)
 JOURNAL MEDLINE 21481677
 PUBMED 11597504
 REFERENCE 2 (bases 1 to 1140)
 Stracke, R. and Weishaar, B.
 Direct Submission
 Submitted (10-JUN-2001) Dept. Plant Breeding and Yield Physiology,
 Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg
 10, Koeln D-50829, Germany
 3 (bases 1 to 1140)
 Stracke, R. and Weishaar, B.
 Direct Submission
 Submitted (29-AUG-2001) Dept. Plant Breeding and Yield Physiology,
 Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg
 10, Koeln D-50829, Germany
 Sequence update by submitter
 On Aug 30, 2001 this sequence version replaced gi:13430155.
 REMARK
 COMMENT
 FEATURES
 LOCATION/Qualifiers

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 8, 2003, 10:30:00 ; Search time 223 Seconds

(Without alignments)
2080.321 Million cell updates/sec

Title: US-10-021-811-36

Perfect score: 1138
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALL=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	759.5	66.7	862	21 AAC57336	Eucalyptus grandis
2	671	59.0	910	21 AAC40587	Arabidopsis thalia
3	667	58.6	908	21 AAC48506	Arabidopsis thalia
4	625.5	55.0	907	21 AAC57337	Eucalyptus grandis
5	585	51.4	621	21 AAC41714	Arabidopsis thalia
6	585	51.4	1127	21 AAC37953	Arabidopsis thalia
7	540	47.5	673	21 AAC36197	Eucalyptus grandis
8	539	47.4	1137	22 AAD05784	Arabidopsis thalia
9	523.5	46.0	981	24 ABK65252	Arabidopsis thalia
10	510	44.8	972	22 AAB87724	Pepermint plant o
11	495	43.5	626	22 AAC57194	Eucalyptus grandis
12	478	42.0	524	21 AAC57194	Arabidopsis thalia
13	475	41.7	837	20 AAC25572	Arabidopsis thalia
14	459	40.3	959	21 AAC44894	Eucalyptus grandis
15	421	37.0	389	21 AAC56152	Eucalyptus grandis
16	421	37.0	417	21 AAC56774	Pinus radiata tran
17	410.5	36.1	516	21 AAC56352	Pinus radiata tran
18	410.5	36.1	516	21 AAC56457	Arabidopsis thalia
19	406.5	35.7	1384	21 AAC42228	Arabidopsis thalia
20	406	35.7	660	24 ABK65183	Pinus radiata tran
21	405.5	35.6	542	21 AAC56434	Pinus radiata tran
22	404.5	35.5	389	21 AAC56837	Cotton transcripti
23	404	35.5	1081	22 AAF90596	CDNA sequence of a
24	402.5	35.4	1820	21 AAZ46048	Nucleotide sequenc
25	402.5	35.4	1820	22 AAB28336	Arabidopsis thalia
26	400.5	35.2	774	21 AAC42662	Arabidopsis thalia
27	397.5	34.9	1209	22 AAD05748	Arabidopsis thalia
28	397.5	34.9	1209	24 ABK65181	Arabidopsis thalia
29	396.5	34.8	1006	22 AAF90594	Cotton transcripti
30	396	34.8	2220	18 AAT60744	Pinus radiata tran
31	392	34.4	1218	21 AAC57346	Arabidopsis thalia
32	391.5	34.4	612	24 ABK65317	Arabidopsis thalia
33	390.5	34.3	800	24 ABK65247	Pinus radiata tran
34	390	34.3	526	21 AAC57245	Arabidopsis thalia
35	387	34.0	1369	22 AAD05764	Arabidopsis thalia
36	386.5	34.0	1825	21 AAC44207	Arabidopsis thalia
37	386	33.9	2352	18 AAT60745	Rice gibberellin-r
38	385	33.8	1062	21 AAC43611	Arabidopsis thalia
39	385	33.8	1087	22 AAD06456	Arabidopsis thalia
40	384	33.7	1081	24 ABK65248	Arabidopsis thalia
41	383.5	33.7	949	22 AAF85188	Nucleotide sequenc
42	383.5	33.7	2521	20 AAX25571	Arabidopsis thalia
43	383	33.7	573	21 AAC57325	Pinus radiata tran
44	382.5	33.6	843	21 AAC43054	Arabidopsis thalia
45	382.5	33.6	1044	24 AEN98399	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAC57336
ID AAC57336 standard; DNA; 862 BP.

XX 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor DNA sequence #773.

XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;

KM poplar; sweetgum; teak; mahogany; bzlp; G-box binding factor;

KM basic helix-loop-helix zipper; homeotic; homeodomain; MADS;

KM homeodomain zipper; LIM domain; AP2; ERBS; zinc finger domain;

XX type 2 Cys2His2; CCAAT box element; MYB; ss.

XX Eucalyptus grandis.

XX

Accession	Sequence	Length	Matches	Conservative	Mismatches	Indels	Gaps
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XX	09-MAR-2000; 2000MO-US06112.	862	152	9	29	21	5
XX	11-MAR-1999; 99US-0266513.	862	152	9	29	21	5
XX	18-AUG-1999; 99US-0149485.	862	152	9	29	21	5
XX	(GENE-) GENESIS RES & DEV CORP LTD.	862	152	9	29	21	5
PA	(FLET-) FLETCHER CHALLENGE FORESTS LTD.	862	152	9	29	21	5
XX	Wood M, McGrath A, Shenk MA, Glenn M;	862	152	9	29	21	5
XX	WPI; 2000-579369/54.	862	152	9	29	21	5
XX	New isolated polynucleotide encoding a plant transcription factor for	862	152	9	29	21	5
XX	producing a plant e.g. a woody plant, preferably eucalyptus or pine,	862	152	9	29	21	5
XX	having modified gene expression or modified activity of a polypeptide	862	152	9	29	21	5
XX	-	862	152	9	29	21	5
XX	Claim 1; Page 649; 747pp; English.	862	152	9	29	21	5
XX	The present invention relates to novel plant transcription factors from	862	152	9	29	21	5
XX	CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding	862	152	9	29	21	5
XX	sequence for one such transcription factor. The transcription factor may	862	152	9	29	21	5
XX	be used to produce a plant having modified gene expression such as a	862	152	9	29	21	5
XX	woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or	862	152	9	29	21	5
XX	managery species or to modify the activity of a polypeptide in a plant.	862	152	9	29	21	5
XX	CC The transcription factors of the present invention are members from the	862	152	9	29	21	5
XX	following families of regulatory proteins: bzip, bzip family of G-box	862	152	9	29	21	5
XX	binding factors, basic helix-loop-helix zipper,	862	152	9	29	21	5
XX	CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2	862	152	9	29	21	5
XX	and ERBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements	862	152	9	29	21	5
XX	and MYB.	862	152	9	29	21	5
XX	Sequence 862 BP; 268 A; 187 C; 213 G; 194 T; 0 other;	862	152	9	29	21	5
XX	Alignment Scores:	862	152	9	29	21	5
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XX	Score: 759.50	862	152	9	29	21	5
XX	Percent Similarity: 76.30%	862	152	9	29	21	5
XX	Best Local Similarity: 72.04%	862	152	9	29	21	5
XX	Query Match: 66.74%	862	152	9	29	21	5
XX	DB: 21	862	152	9	29	21	5
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QY	19 ProTPRtMetGInGInAspLeuIleIleMetSerntYrIleIaIaEnHISGlyGInGly 38	862	152	9	29	21	5
Db	91 CCGTGAAGACGAGAGAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 150	862	152	9	29	21	5
QY	39 ValTPaenSerLeuAlaIyAlaIaIaGlyLeuIySArGInGlyIySerCyArGLeu 58	862	152	9	29	21	5
Db	151 AATGGAACTCCCTTAAGCCAAAGCTGCTGTCTTAAACGTACCGGGAAGAGTGTCCGCTC 210	862	152	9	29	21	5
QY	59 AcGTPLaEuAenYrIleuArGProAspVaIaArGInGInaEnIleTPRProGInGInGIn 78	862	152	9	29	21	5
Db	211 CAGTGGCTGAACATCT 270	862	152	9	29	21	5
QY	79 LeuLeuIleMetGInLeuHISAlaIySTrPGIyASnaRGTTPSerIyIleAlaIySHIS 98	862	152	9	29	21	5
Db	271 CTCCTGATCATGGAATGTCATGCCAAGGGGAAACAGGTGTCTTAAATTGCCAAGCAT 330	862	152	9	29	21	5
QY	99 LeuTPROGInArgTrAspAsnGInIleIyAsnYrTrTPaRtghArGIn						

Db	391	ATCAGCAAGCAGAGCGCTTCTCTCGTACGAGCTCCAGATGAGTAT	438
Qy	139	GlnAlaSerThSerHisValSerThMetLeuIleuProMetGluMetTyr--SerPro	157
Db	439	CAGGCAAGCAGCAGGCAATGTCACGATGCCAGAGCCATGAGACCTTACGACTACCG	498
Qy	158	ProCysTyrGlnGly-----MetIleuGluProPheSerThGlnPheProThrIleasn	175
Db	499	CCGTATCTCCAGGCAAGCAGACACATGAGCGCTTGGCCGGTGAATTGTGGTC-----	552
Qy	176	ProAspGlnSerSerCysCysThrAsnAspAsnAsnIleasnTyrTTPSerMetGlu	195
Db	553	-----GAGTCAATATGAAGCCTTCTGGAGCATGAC	582
Qy	196	AapSerTTPSerMetGlnLeuLeuAsnGlyAap	206
Db	583	GATCTTGGTCTATGCACTGATCTACTCAATGGGAT	615
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XX	DT	17-OCT-2000 (first entry)	
XX	DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 28847.	
XX	KM	Hybridisation assay; genetic mapping; gene expression control;	
XX	KW	protein identification; signal transduction pathway;	
XX	KW	metabolic pathway; promoter; termination sequence; ss.	
OS		Arabidopsis thaliana.	
XX	PM	EP1033405-A2.	
XX	PD	06-SEP-2000.	
XX	PF	25-FEB-2000; 2000EP-0301439.	
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
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PR	20-MAY-1999;	99US-0135124.	
PR	21-MAY-1999;	99US-0135533.	
PR	24-MAY-1999;	99US-0135629.	

PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
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PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142350.
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PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 28-OC³-1999; 99US-0161993.
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Alignment Scores:

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Score:	671.00	Matches:	133
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Query Match:	58.96%	Indels:	8
DB:	21	Gaps:	4

US-10-021-811-36 (1-206) x AAC40587 (1-910)

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QY 19 ProTrpThrMetGluGluAspLeuIleLeuMetAsnTrpIleAlaAsnHisGlyGluGly 38
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QY 39 ValTrpAsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeu 58
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QY 59 ArgTrpLeuAsnTrpLeuArgProAspValArgArgGlyAsnIleThrProGluGln 78
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QY 79 LeuLeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHis 98
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QY 99 LeuProGlyArgTrpAspAsnGluIleLysAsnTrpArgTrpArgIleGlnLysHis 118
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QY 139 GlnAlaSerThrSerHisVal---SerThrMetAlaGluProMetGluMetLysSerPro 157
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DB 530 CATGCGACAAAGAGCCATGTCATGATGATACATGACAAACCATGGATATGTTCCCA 589
QY 158 ProCysArgGlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsn----- 175
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DB 590 ACGACGTCGATCAACATGCCAGCAATATTATATCAGCAGCTTAATTATGTAATATGTCG 649
QY 176 ProAspGlnSerSerCys-----CysThrAsnAspAsnAsnIleAsnTrp 192
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RESULT 3
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AC AAC48506;
XX AAC48506;
XX 18-OCT-2000 (first entry)
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XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX
XX
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PN EP1033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
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PR 05-MAR-1999; 99US-0123180.
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PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
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Best Local Similarity: 61.68% Mismatches: 51
Query Match: 58.61% Indels: 8
DB: 21 Gaps: 4

US-10-021-811-36 (1-206) x AAC48506 (1-908)

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QY 19 ProTyrThrMetGlnGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGlnGly 38
DB 168 CCATGACCATGGAAGAAATTTGATTCTCATCAATTATATGCGCAATCATGTGAAGGT 227
QY 39 ValTyrAsnSerLeuAlaLysAlaIleGlyLeuLysArgAsnGlyLysSerCysArgLeu 58
DB 228 GTTTGAACTCTCTCCCAAACTTCGAGACTTAAACGACCGGAAAGTTGCCGCTC 287
QY 59 ArgTyrLeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGln 78
DB 288 CGGTGGCTGAACCTACCTCCGACCTGATGTGCGACGGGAAATTCACACAGAAAGACG 347
QY 79 LeuLeuIleMetGluLeuHisAlaLysTyrGlyAsnArgTyrSerLysIleAlaLysHis 98
DB 348 CTCACCATCATGGAACCTCATGCAAAATGGGGAAATAGGTGTGTCAAAATTGCCAAGCAT 407
QY 99 LeuProGlyValArgThrAspAsnGluIleLysAsnTyrTyrArgIleArgIleGlnLysHis 118

KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX EPI033405-A2.
PN
XX 06-SEP-2000.
PD
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PF 25-FEB-2000; 2000EP-0301439.
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Alignment Scores:

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Pred. No.: 2,29e-55 Length: 621
Score: 585.00 Matches: 121
Percent Similarity: 65.14% Conservative: 21
Best Local Similarity: 55.50% Mismatches: 44
Query Match: 51.41% Indels: 32
DB: 21 Gaps: 6
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US-10-021-811-36 (1-206) x AAC41714 (1-621)

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QY 1 MetAspIySylGInGInCysLys-----ThisSerIlnAspProGlu----- 14
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QY 15 ValArgIySglYProTPThrMetGluGluAspLeuIleLeuMetCAsnYrIleAlaAsn 34
Db 73 GTGAGAAAGAGACTTGAGCATATGAGAAAGATTTCATCTCTTTAATTACATCTTAAT 132
QY 35 HisGluGluGluValITPAnSerLeuAlaIleAlaIleLeuIleuIleuIleuIleu 54
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QY 55 SarCysArgIleuArgITPLeuAsnYrLeuArgProAspValArgArgIleuIleuIleu 74
Db 193 AATTGTGGCTCGGTGTGTAATCTCCGACCAAGATGTGGGAGGAGAAACATTAACC 252
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QY 75 ProGluGluGluLeuLeuIleMetGluLeuHisAlaIySTyrGlyAsnArgTTrpSerIys 94
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QY 95 IleAlaIleHisLeuProGluYrGThrAspAenGluIleIleYAsnYrITPArgThArg 114
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QY 115 IleGluIleHisIleIleYsGluAlaIleu-----AspHeGluGluIlnSerSer 130
Db 373 ATTCAGAGACACATGTAAGATGTCATCGGAAATATATGATGATCATCATCATTTGTTCC 432
QY 131 AsnAsnSerGluIleAsn-----AspHisGluAlaSerThrSerHisValSerThrMet 148
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QY 149 AlaGluProMetGluMetIySerProProCysYrITyGInGluMetLeuGluProPheSer 168
Db 493 GCTGAGAGCTTCTCT-----CAGGCGAAGACG 519
QY 169 ThrGluPheProThrIleAsnProAspIlnSerSerCysYrThrAsnAspAsnAsn 188
Db 520 ACGACGTTAATATGTGTC-----GAACAACAGTCAAAC 552
QY 189 IleAsnYrITrPserMetGluAspSerITrPserMetGluLeuAsnGlyAsp 206
Db 553 GAGAACTTACTGAGACGTTGAGATCTGTGCCCGCTCACTGCTTAATGTGTAC 606
RESULT 6
AAC37953
ID AAC37953 standard; DNA; 1127 BP.
XX
AC AAC37953;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 19258.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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Db 182 GAGACGCTTTGATCTCGAGCTCCATTCCCGCTGGGGCAATGATGTTGAAGATCGG 241
Qy 97 LysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGln 116
Db 242 CAACACTTTGGCGGGGAGAGACGACAGATCAAGAACTACTAGGGAACCGGGTGGAG 301
Qy 117 LysHisIleLysGlnAlaGluAsnPheGlnGlnSerSerAsnAsnSerGluIleAsn 136
Db 302 AAGCAGCGCAAGCAGCTC-----AAATGTAGCTCAACAGCAGAGCTTCAAG 349
Qy 137 AspHis-----GlnAsnSerThrSer 143
Db 350 GAGCGCATGAATACTCTGTGATGCCAGAGCTGTGAGAGATCCAGCGCTCGGC 409
Qy 144 HisValSerThr-----MetAlaGluProMetGluMetTyrSer 156
Db 410 TGTGTCTCGACCGTACTGTGCGCGCGCGCATGGCAAGCCCAACAAATGGCCACC 469
Qy 157 -----ProProCysTyrGlnGlyMetLeuGlu 165
Db 470 ACCGACAGATCCAAATCGCGCGCATGCTTCCCGCGCGCTGGCGGCATGGCGGC 529
Qy 166 ProPheSer-----ThrGlnPheProThrIleAsnProAspGlnSerSerCys 181
Db 530 GACTTCAGGGGGCGGCGGAGATGATGAGCGCCAGCTACAGACCCCGGAGAACTCTGC 589
Qy 182 CysThrAsnAspAsnAsnAsnIleAsnTyrTrpSerMetGluAspSerTyrSerMetGln 201
Db 590 ACGACG-----GCGTCTTCCGACTGATTCGATTCGGTGGCAG 622
Qy 202 Leu 202
Db 623 GTC 625

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RESULT 8

AAAD05784 ID AAD05784 standard; cDNA; 1137 BP.

AC AAD05784;

DT 31-JUL-2001 (first entry)

DE Arabidopsis thaliana transcription factor, G1324 cDNA.

KM Transcription factor; biochemical characteristic; controlling element;
 KW structural characteristic; developmental characteristic; gene therapy;
 KW agricultural biotechnology; plant trait modification; ss.

XX Arabidopsis thaliana.

XX Key Location/Qualifiers

FT CDS 54..914

FT /tag= a

FT /product= "Transcription factor, G1324"

PN WO200136597-A1.

PD 25-MAY-2001.

PF 14-NOV-2000; 2000WO-US31344.

PR 17-NOV-1999; 99US-0166228.

PR 17-APR-2000; 2000US-0197899.

PR 22-AUG-2000; 2000US-0227439.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.

PA (CREE/) CREELMAN R.

PA (YUGG/) YU G.

PA (ADAM/) ADAM L.

PA (RIEC/) RIECHMANN J L.

PA (HEAR/) HEARD J.

PA (SAMA/) SAMAH R.

PA (PLIG/) PILGRIM M.

PA (PINE/) PINEDA O.
 PA (JIANG/) JIANG C.
 XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R,
 PI Pilgrim M, Pineda O, Jiang C;
 XX WPI, 2001-335999/35.
 DR P-PSDB; AAE01900.

PT Nucleic acids encoding plant transcription factor polypeptides, useful
 for altering the biochemical characteristics of plants e.g. corn,
 potato and cotton plants -

PS Claim 4; Page 87-88; 127pp; English.

CC The present sequence is Arabidopsis thaliana transcription factor,
 CC G1324 cDNA. The transcription factor is used for altering a plant's
 CC biochemical characteristics. The transcription factor may be used to
 CC alter the structure and developmental characteristics of plants such as
 CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,
 CC alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry,
 CC raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,
 CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers,
 CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,
 CC roseaceous fruits and/or vegetable brassicas. Transcription factors are
 CC key controlling elements of biological pathways and altering expression
 CC levels of 1 or more transcription factors can change entire biological
 CC pathways in an organism. Therefore manipulating transcription factor
 CC levels in plants offers great potential in agricultural biotechnology
 CC for modifying a plant's traits. Transcription factor cDNA is useful in
 CC gene therapy.

XX SQ Sequence 1137 BP; 378 A; 213 C; 233 G; 313 T; 0 other;

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
539.00	539.00	1137	107
Percent Similarity:	66.18%	Conservative:	28
Best Local Similarity:	52.45%	Mismatches:	43
Query Match:	47.36%	Indels:	26
DB:	22	Gaps:	5

US-10-021-811-36 (1-206) x AAD05784 (1-1137)

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Qy 1 MetAspLysLeuGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTyr 20
Db 66 ATGAAATAAATAAAGAGAGCTTCAAGAAAGTGAAGAACTAAGAAAGAGGCTTGG 125
Qy 21 ThrMetGluGluAspLeuIleLeuMetCysTyrIleAlaAsnHisGlyGluGlyValTyr 40
Db 126 ACTTTGAGAGAAAGACACACTTCTCAAAATTACATCTCCATTAACGATGAGGTTGG 185
Qy 41 AsnSerLeuAlaLysAlaIleGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTyr 60
Db 186 AATCAGCTGCCAAAGTCTGAGCTTAAGAGAACTGGGAAAGTTGATGATGAGATGG 245
Qy 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGlnGlnLeu 80
Db 246 TTGAATTACTTGAACCCGACATTAAGACGAGGGAATCTTACTCCACAGAAACAGCTTTG 305
Qy 81 IleMetGluLeuHisAlaLysTyrGlyAsnArgTyrSerLysIleAlaLysHisLeuPro 100
Db 306 ATCTTGAGCTTCACTCACTTAATGCGGTATAGTGTGCTCAAAATTTGCAACAGATTGGCA 365
Qy 101 GlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIleLys 120
Db 366 GGAAGAACGATTAAGAGATCAAGAACTATTGGAAGAACAGAGTTCAAAACAGCTGCT 425
Qy 121 GlnAlaGluAsnPheGlnGlnGlnSerSerAsnAsnSerGluIleAsnAspHisGlnAla 140
Db 426 CAACCTC--AACTCGAA-----TCTTAACAGGCAACAACTTCTTGGAC--GCTGTT 470
Qy 141 SerThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProCysTyr 160

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RESULT 11

AAH87724
ID AAH87724 standard; cDNA; 626 BP.
XX
AC AAH87724;
XX
DT 25-SEP-2001 (first entry)
XX
DE Peppermint plant oil gland expressed cDNA 80.
XX
KW Peppermint; plant oil gland cell; terpenoid essential oil; resin;
KM genetic mapping; antisense suppression; recombinant expression; ss.
XX
OS Mentha x piperita.
XX
PN M02001.33319-A1.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02567.
XX
PR 20-JAN-2000; 2000US-0177264.
XX
PS (CROT/1) CROTEAU R. B.
PA (LANG/1) LANGE B. M.
PA (WILD/1) WILDUNG M. R.
XX
PI Croteau RB, Lange BM, Wildung MR;
XX
DR WPI; 2001-488706/53.
XX
PT New nucleic acid molecules corresponding to mRNA molecules expressed in
PT peppermint oil glands for enhancing expression of plant oil gland cell
PT proteins -
XX
PS Claim 1; Page 108; 25pp; English.
XX
CC The invention relates to nucleic acid molecules (AAH87645-AAH88116) that
CC correspond to all or part of a mRNA molecule expressed in plant oil
CC gland cells, especially peppermint and plant oil glands that produce
CC terpenoid essential oils and resins. The nucleic acids are useful for
CC genetically mapping a plant genome for genes expressed in plant oil
CC gland cells and to suppress (for example by antisense suppression) or
CC enhance their expression (for example by genetically transforming a
CC plant cell with a replicable expression vector that expresses one or more
CC proteins naturally expressed in plant oil gland cells). The nucleic acids
CC are also useful for recombinant expression of plant oil gland proteins
CC required for terpenoid essential oil and/or resin production in bacterial
CC and/or yeast cells.
XX
SQ Sequence 626 BP; 187 A; 158 C; 163 G; 118 T; 0 other;

Alignment Scores:

Pred. No.: 2.16e-45 Length: 626
Score: 495.00 Matches: 98
Percent Similarity: 69.59% Conservative: 21
Best Local Similarity: 57.31% Mismatches: 23
Query Match: 43.50% Indels: 29
DB: 22 Gaps: 4

US-10-021-811-36 (1-206) x AAH87724 (1-626)

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Db 116 AGGTGTGAGAGAGAGAGAGAGAGAAATATGATGAGGTGAGAGAGAGGCGCGTGG 175
OY 21 ThrMetGluGluAspLeuIleuMetSerAntyrrilealaasnhsigluGluGlyValTyr 40
Db 176 AAGATTGAGAGAGACTTACCTATCACTACATCGCCCACTACAGGAGAGGCGCATGG 235
OY 41 AansrLeuAlaLysAlaAlaGlyLeuLysArgLysnglyLysSerCysArgLeuArgTyr 60

Db 236 AACTCTGTGCTCGCTCAGACAGCCCTCAACAGAACTCGAAGAGCTGCAGACTGAGATCG 295
OY 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGluLeu 80
Db 296 CTGAACTATCTCGCCCGCATGTCCGACCTGCGCAACATCACTTGAAGAGAGAGCTTTTG 355
OY 81 IleMetGluLeuHisAlaLysTrpGlyAsnArgTyrSerIleAlaLysHisLeuPro 100
Db 356 ATTCTGACCTCCATCTCTGATGAGGCAACAGTGGTGGAAATGCGCAGATCTGCCG 415
OY 101 GlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGluLysHisIleLys 120
Db 416 GGAAGAACTGACTACGAACTAAAGAACTGAGAAACAAAGAGTCA----- 463
OY 121 GlnAlaGluAsnPhenGlnGlnSerSerAsnAsnSerGluIleAsnAspHisGlnAla 140
Db 464 -----AACATGCAAGCAAGCTCAAT-----GTACGTCACAGACAGCA 502
OY 141 -SerThrSerHisVal-----SerThrMet 148
Db 503 TTCAGAGACCCATGCCCTTACCTTTGATGCTTACGCTGATGAGAAATCCAAAGCACTTC 562
OY 148 talagluProMetGluMetLysSerProPro 158
Db 563 TGCACTGCTGCTGCTCGCGGCTCGGCTTCG 593
RESULT 12
AAC57194
ID AAC57194 standard; DNA; 524 BP.
XX
AC AAC57194;
XX
DT 25-JAN-2001 (first entry)
XX
DE Eucalyptus grandis transcription factor DNA sequence #700.
XX
KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
KW basic helix-loop-helix zipper; homeotic; homeobox; MADS;
KW homeodomain zipper; LIM domain; AP2; ERBs; zinc finger domain;
KW type 2 Cys2His2; CCAAT box element; MYB; ss.
XX
OS Eucalyptus grandis.
XX
PN M0200053724-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06112.
XX
PR 11-MAR-1999; 99US-0266513.
PR 18-AUG-1999; 99US-0149485.
XX
PA (GENE-) GENESTIS RES & DEV CORP LTD.
PA (FLEET-) FLEETCHER CHALLENGE FORESTS LTD.
XX
PI Wood M, McGrath A, Shenk MA, Glenn M;
XX
DR WPI; 2000-579369/54.
XX
PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
PT -
XX
PS Claim 1; Pages 614-615; 747bp; English.
XX
CC The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.

PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150560.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161970.
 PR 28-OCT-1999; 99US-0161982.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Alignment Scores:

Pred. No.: 3.8e-41
 Score: 459.00
 Percent Similarity: 54.22%
 Best Local Similarity: 41.78%
 Query Match: 40.33%

Length: 959
 Matches: 94
 Conservative: 28
 Mismatches: 57
 Indels: 46
 Gaps: 5

US-10-021-811-36 (1-206) x AAC44894 (1-959)

Oy 16 ArglysglyProTTPThMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHis 35

Db 204 AGAAAGAGGCGCTTGGACCTGCTGAGAGAGACCGGCTTTGATTCATTATGACGCTTGAC 263
 Oy 36 G|I|G|I|G|I|Y|V|A|T|T|P|A|S|S|E|L|E|A|I|A|A|I|A|L|Y|E|U|Y|S|A|S|A|N|G|I|Y|L|Y|S|E| 55
 Db 264 GGTAAAGGCGCATGGAACCTCTGTGGCAGGCTCGGGGTTGAAAGAAATGGGAAAAAGC 323
 Oy 56 CysArgLeuArgTTPLeuAsnTyrLeuArgProAspValArgArgIleAsnIleThrPro 75
 Db 324 TGCAGGTTTAAATGGTGTAACTTAACCTTAAGACAGACCTCAAGAGAGGACAAATCACTCCT 383
 Oy 76 GluGluGlnLeuLeuIleMetGluLeuHisAlaIlySTTPGlyAsnArgTTPSerIle 95
 Db 384 CATGAAGAAACCATTTATCTTGAAGTACATGCTAAGTGGGCAATAGTGTCCACGATT 443
 Oy 96 AlAlYSHISLIEuProGlyArgThrAspAsnGluIleYsAsnTyrTPArgTThArgIle 115
 Db 444 GACGTAAGTTTACCGGAGAGAGACAGACAGAAATCAAGAACTTATGGCAACCATTC 503
 Oy 116 GlnYSHISLIElysglnIleAsn----- 124
 Db 504 AAGAAAGAGAGAGAGTCTCCAACTTAACAGTCCGAGAGAACAAAGAACCAATCTTGAG 563
 Oy 125 -----PheGlnGlnGln----- 128
 Db 564 AGGCACCAATTTACAGACCAAGACAAATGAGTTGACAGACAAACAGTTCCTTCAA 623
 Oy 129 -----SerSerAsnSer 133
 Db 624 TTCATCAATCGACATGAAATAATCATGCTGCTTACTAGTACGACAAACAAATGCT 683
 Oy 134 GluIleAsnAspHisglnAlaSerThrSerHisValSerThrMetAlaGluProMetGlu 153
 Db 684 GATAACACCTTCAGACAGTACAGTACGCAAGTGGAGCATTTATGTACTTCATCAG 743
 Oy 134 MetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSerThr---GlnPhePro 172
 Db 744 ATCAACACATTCACAAACAACTTCTGT--TGTAAACCAATATGTAACGGTATTACCG 800
 Oy 173 ThrIleAsnProAspGlnSerSerCysThrAsnAspAsnAsnIle-----Asn 190
 Db 801 GTGGTTCGGGTACAAATACCTGAGGCTAATGTAATGAATTAACGCAATTTGGAGCGT 860
 Oy 191 TyrTTPSerMetGlu 195
 Db 861 TTATGGAATCTGGAT 875
 RESULT 15
 AAC56152
 ID AAC56152 standard; DNA; 389 BP.
 XX
 AC AAC56152;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Eucalyptus grandis transcription factor DNA sequence #283.
 XX
 KW plant; transcription factor; gene expression; eucalyptus; pine; acacia;
 KW poplar; sweetgum; leak; mahogany; bzlp; G-box binding factor;
 KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
 KW homeodomain zipper; LIM domain; AP2; ERBBS; zinc finger domain;
 KW type 2 Cys2His2; CCAAT box element; MYB; sb.
 XX
 OS Eucalyptus grandis.
 XX
 PN WO200053724-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US06112.
 XX
 PR 11-MAR-1999; 99US-0266513.
 PR 18-AUG-1999; 99US-0149485.

XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Wood M, McGrath A, Shenk MA, Glenn M,
PI WPI: 2000-579369/54.
XX
XX New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide
PT
XX
XX Claim 1; Page 120; 747pp; English.
XX
XX The present invention relates to novel plant transcription factors from
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding
CC sequence for one such transcription factor. The transcription factor may
CC be used to produce a plant having modified gene expression such as a
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
CC mahogany species or to modify the activity of a polypeptide in a plant.
CC The transcription factors of the present invention are members from the
CC following families of regulatory proteins: bZIP, bZIP family of G-box
CC binding factors, basic helix-loop-helix zipper,
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
CC and ERBBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements
CC and MYB.
XX
XX SQ Sequence 389 BP; 112 A; 102 C; 97 G; 78 T; 0 other;

XX Alignment Scores:
XX Pred. No: 1,75e-37 Length: 389
XX Score: 421.00 Matches: 81
XX Percent Similarity: 88.17% Conservative: 1
XX Best Local Similarity: 87.10% Mismatches: 9
XX Query Match: 36.99% Indels: 2
XX DB: 21 Gaps: 1

XX US-10-021-811-36 (1-206) x AAC56152 (1-389)

QY 1 MetAspIySlyS-----GInGInCySlySthSergInaSPProGIuValArgLySgLy 18
Db 44 ATGGACAAAGAGCCAGACGACAGTGTAGTCCCAAGATGTCGAGTGAAGAAAAGGG 103
QY 19 ProTrpThrmGtGluGluAspLeuIleuMetAsnTrpIleAlaAsnHisGlyGluGly 38
Db 104 CCGTGGACGATGAGAGGATCTCATCTCATCACTAAGGATCAAGGCGAAGGC 163
QY 39 ValTrpAsnSerIeuAlaIySAlaIaGlyLeuIySArgAsnGlyIySerCySArgLeu 58
Db 164 AGTTGGAACCTCCCTAGCCAAAGCTGCTGTCTTAAACGTACCGGAAAGATTGTCCGGCTC 223
QY 59 ArgTrpLeuAsnTrpIeuArgProAspValArgArgIyAsnIleThrProGIuGluGlu 78
Db 224 CCGTGGCTGAACATATCTGCGACCCGAGCTCCGAGAGGCAACATCACTACTGAGAGCAG 283
QY 79 IeuIeuIleMetGluIeuHisAlaIySTPGLyAsnArg 91
Db 284 CTCTGATCATGGAACATGATGCCAAGTGGGGAACACAG 322

Search completed: February 8, 2003, 11:12:19
Job time : 226 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 8, 2003, 11:07:40 ; Search time 48 Seconds

(without alignments)
1316.154 Million cell updates/sec

Title: US-10-021-811-36

Perfect score: 1138
Sequence: 1 MFKKQCKTSQDPYVKKGPW.....NNINYSWEDSWSMQLNCD 206

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q/cgn2_1/USFTO.spool/US10021811/runat.03022003.111222.25655/app.query.fasta_1.391
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=rni -MINMATCH=0.1 -DOOPCL=0
-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCMATCH=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10021811 @CGN 1.1 25 @runat.03022003.111222.25655 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEIOBRY -NEG_SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARM TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Issued Patents NA:*
2: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	396	34.8	2220	4 US-08-997-251-1	Sequence 1, Appl1
2	386	33.9	2352	4 US-08-997-251-3	Sequence 3, Appl1
3	382.5	33.6	1344	2 US-08-722-6268-1	Sequence 1, Appl1
4	305.5	26.8	1035	5 PCT-US93-06251-90	Sequence 90, Appl1
5	305.5	26.8	3225	1 US-08-306-6918-45	Sequence 45, Appl1
6	305.5	26.8	3225	5 PCT-US93-06251-91	Sequence 91, Appl1
7	305.5	26.8	3230	5 PCT-US93-06251-89	Sequence 89, Appl1
8	296	26.0	1897	4 US-09-167-322-10	Sequence 10, Appl1
9	293	25.7	4880	4 US-09-402-929-5	Sequence 5, Appl1
10	291.5	25.6	3602	4 US-09-402-929-1	Sequence 1, Appl1
11	291.5	25.6	6775	4 US-09-402-929-4	Sequence 4, Appl1
12	271.5	23.9	2638	1 US-08-306-6918-46	Sequence 46, Appl1

13	248	21.8	4059	2 US-08-485-139-1	Sequence 1, Appl1
14	248	21.8	4059	3 US-08-750-357-1	Sequence 1, Appl1
15	248	21.8	4824	2 US-08-485-139-5	Sequence 5, Appl1
16	248	21.8	4824	3 US-08-750-357-5	Sequence 5, Appl1
17	195.5	16.3	469	3 US-09-008-979A-2	Sequence 2, Appl1
18	185.5	16.3	469	4 US-09-460-618-2	Sequence 2, Appl1
19	185.5	16.3	469	4 US-09-310-235B-2	Sequence 2, Appl1
20	165.5	14.5	5889	4 US-09-402-929-3	Sequence 3, Appl1
21	125	11.0	785	3 US-09-008-979A-6	Sequence 6, Appl1
22	125	11.0	785	4 US-09-460-618-6	Sequence 6, Appl1
23	125	11.0	785	4 US-09-310-235B-6	Sequence 6, Appl1
24	119	10.5	2837	4 US-09-156-316-11	Sequence 11, Appl1
25	105.5	9.3	1116	4 US-08-928-941D-17	Sequence 17, Appl1
26	105.5	9.3	1116	4 US-09-280-590A-17	Sequence 17, Appl1
27	105.5	9.3	2903	4 US-08-928-941D-2	Sequence 2, Appl1
28	105.5	9.3	2903	4 US-08-928-941D-3	Sequence 3, Appl1
29	105.5	9.3	2903	4 US-09-280-590A-2	Sequence 2, Appl1
30	105.5	9.3	2903	4 US-09-280-590A-3	Sequence 3, Appl1
31	105.5	9.3	3767	4 US-08-928-941D-28	Sequence 28, Appl1
32	105.5	9.3	3767	4 US-08-928-941D-30	Sequence 30, Appl1
33	105.5	9.3	3767	4 US-09-280-590A-28	Sequence 28, Appl1
34	105.5	9.3	3767	4 US-09-280-590A-30	Sequence 30, Appl1
35	96.5	8.5	282	2 US-08-814-030-2	Sequence 2, Appl1
36	93	8.2	336	1 US-08-248-474-105	Sequence 105, App
37	93	8.2	336	3 US-08-756-849-105	Sequence 105, App
38	84.5	7.4	3834	4 US-09-221-017B-663	Sequence 663, Appl
39	83.5	7.3	2581	4 US-09-370-838-66	Sequence 66, Appl
40	82.5	7.2	3642	3 US-08-946-026-16	Sequence 16, Appl
41	81.5	7.2	3627	1 US-08-447-500-23	Sequence 23, Appl
42	81.5	7.2	3627	1 US-08-454-097-23	Sequence 23, Appl
43	81.5	7.2	3627	1 US-08-453-866-23	Sequence 23, Appl
44	81.5	7.2	3627	3 US-08-185-359-23	Sequence 23, Appl
45	81.5	7.2	3628	1 US-08-468-036-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-997-251-1
Sequence 1, Application US/08997251
Parent No. 6271440
GENERAL INFORMATION:
APPLICANT: GUBLER, FRANZ J.
APPLICANT: JACOBSEN, JOHN V.
TITLE OF INVENTION: PLANT REGULATORY PROTEINS III
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Boulevard
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,251
FILING DATE: 23-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: WO AU96/00383
FILING DATE: 21-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU EN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU EN3779/95
FILING DATE: 23-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P.

Qy 93 SerlylealalyshisleuproglyArgThraspansglulleysaenlyrTyrParg 112
Db 747 GCTGGATGCGCCCTCTATTGCCAGGGCGCATATATAAATAAGATTACTGGAAAT 806
Qy 113 ThrArgllegllyls-----Hisllelys 120
Db 807 ACTGGAATTAAGAGATCCAGCGAGTGGCTTATCCATCTATCTTACCAAGCTTATGCAAT 866
Qy 121 GlnAlaGlunpheglnnglnInserSerAsnAsnSerGluIleAsnAphis 138
Db 867 CAATCTCAATTAAGATGACAGTGTCTCCAGTGAATTTGACTGTGGCGAAT 920
RESULT 3
US-08-722-626B-1
Sequence 1, Application US/08722626B
Patent No. 5939601
GENERAL INFORMATION:
APPLICANT: Yang, Yinong
APPLICANT: Kleesig, Daniel, F.
TITLE OF INVENTION: NOVEL GENES ASSOCIATED WITH ENHANCED
TITLE OF INVENTION: DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,626B
FILING DATE: 27-SEP-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pat Hagan
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 97-0010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 563-4100
TELEFAX: 215 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 148...981
OTHER INFORMATION:
US-08-722-626B-1
Alignment Scores:
Pred. No.: 3.09e-37 Length: 1344
Score: 382.50 Matches: 88
Percent Similarity: 54.38% Conservative: 30
Best Local Similarity: 40.55% Mismatches: 60
Query Match: 33.61% Indels: 39

DB: 2 Gaps: 6
US-10-021-811-36 (1-206) x US-08-722-626B-1 (1-1344)
Qy 15 ValArglysglyProTyrThrMetGlnGluAspLeuIleLeuMetAenlyrIleAlaasn 34
Db 181 CTGAATAAAGGGCCATGGATTCCTCGAAGAGATCATGATTCATCTCTTCAATTCAGAACT 240
Qy 35 HisGlyGlnGlyValTyrAsnSerIleuAlaIleGlyLeuValArgAsnGlylys 54
Db 241 AATGCCATGGCACTGGCGAGCCCTTCCAAACAGCGTGCATTTAGAGATGCGGGAG 300
Qy 55 SerCyAsnGluValTyrLeuAsnTyrIleuArgProAspValArgAsnGlyAsnIleThr 74
Db 301 AGTTCCAGACTGCGGTGAGCAGATATTATTTGGCAGCAGATATAAGAGGGGAAATTTCC 360
Qy 75 ProGlnGlnIleuLeuIleuIleuGlnIleuHisAlaIleTyrGlyAsnArgTyrSerlys 94
Db 361 AAGAAAGAAAGAAAGAAACATTTCAGATTACATGAATGCTTGGCAATGATGGTCTCA 420
Qy 95 IleAlalyshisleuproglyArgThraspansglulleysaenlyrTyrArgThyrArg 114
Db 421 ATAGCAGCAAAATTAACAGAGACAGACATGAATTAATAAATGTTGGCACACCCAC 480
Qy 115 IleGlnlyshislely-----GlnAla 122
Db 481 TTGAAGAAAGAAAGCTCAAGATTATTAAGCTCTCCAGAACTCCAAAGACACTCCAAAGTCC 540
Qy 123 GluAsnPhenGln-----GlnInserSerAsnAsnSerGluIle--- 135
Db 541 AAGATCATGATTTCCAGAGGTCTACTACTTCTGATCATCCAAATATTTGATCTTACT 600
Qy 136 -----AsnAsnHisGlnAla 140
Db 601 ATTATTAATACAAACAAACACATGATAGCCAGGTAGTCTCTTAACCTCAACCCCAAT 660
Qy 141 SerThrSer---HisValSerThrMetAlaGluProMetGluMetTyrSerProProCys 159
Db 661 TCATCTTAAGTACGAAATGCACTGACACACAGTCAGATGATCATCAATAGTGTGAT 720
Qy 160 TyrGlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsnProAspGlnSer 179
Db 721 AAGCAAGAAAGTAATGAGTGC---TCCAGATATTTTCCAGATATGAT-----GAG 768
Qy 180 SerCyAsnThraspansnAsnAsnIleAsnTyrTyrSerMetGluAsp 196
Db 769 AGTTTGGACGCGAGCAATTAACAACGACAAATACTGAGTGAATGAT 819
RESULT 4
PCT-US93-06251-90
Sequence 90, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
NUMBER OF SEQUENCES: 93
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

/ NAME: Digiglo, Frank S.
 / REGISTRATION NUMBER: 31,346
 / REFERENCE/DOCKET NUMBER: 8586
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 516-742-4343
 / TELEFAX: 516-742-4366
 / TELEX: 230 901 SANS UR
 / INFORMATION FOR SEQ ID NO: 90:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1035 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: double
 / TOPOLOGY: linear
 / MOLECULE TYPE: DNA (genomic)
 / PCT-US93-06251-90

Alignment Scores:
 Pred. No.: 5.58e-28 Length: 1035
 Score: 305.50 Matches: 70
 Percent Similarity: 59.34% Conservative: 38
 Best Local Similarity: 38.46% Mismatches: 59
 Query Match: 26.85% Indels: 15
 DB: 5 Gaps: 7

US-10-021-811-36 (1-206) x PCT-US93-06251-90 (1-1035)

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QY 12 AEPProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyr 31
DB 121 AACCTGAGCTCATCAAGGCTCTTGGACCAAGAAAGATCAGAGTATAGAGCTT 180
QY 32 TLeaAaenHISGlyGluGlyValTTPAsnSerLeuAlaLysAlaGlyLeuLys-- 50
DB 181 GTACAGAAATTCAGGTCGAAACGTTGCTGTGTATTTGCCAAG-----CACTTAAAGGGG 234
QY 51 ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuAsgProAspValArgArg 70
DB 235 AGAATTGGAAAACATGATGAGGAGAGGTCATTAACCACTTAATCCAGAGTTAAAGAAA 294
QY 71 GLyAenIleTrpProGluGluGlnLeuLeuIleMetGluLeuHISAlaLysTyrGlyAsn 90
DB 295 ACCTCTCGAGAGAGAGAGAGAGCAAGATTATTACCGACGACCAAGACGCTGGGAGAC 354
QY 91 ArgTyrSerLysIleAlaLysHISLeuProGlyArgThrAspAsnGluIleLysAsnTyr 110
DB 355 AGATGGGCAAGAAATCGCAAGAGCTAGCTGCTGAGCAAGATGATATGCTATCCAGAACAC 414
QY 111 TrpArgThrArgIleGlnLysHISileLysGlnAlaGluAsnPhenGlnGlnSerSer 130
DB 415 TGGAAATTCACAAATGCGTCGGAAGGTGCAAG--GAAGGTATATCTGCAGAGTCTTCA 471
QY 131 AsnAsnSerGlu-----IleAsnAspHISGlnAlaSerThrSerHISValSerThrMet 148
DB 472 AAAGCCAGCCGACGACGAGTGGCCACAAGCTTCCAGAAAGAAAGTCAATTGATGGGTTT 531
QY 149 AlaGluProMetGluMetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSer 168
DB 532 GCTCAG-----GCTCCGCTACAGCTCA-----CTCCCTGCCACT 567
QY 169 ThrGlnPheProTrpTLeAsnProAspGlnSerSerCysCysThrAsnAsnAsnAsn 188
DB 568 GGCAG--CCCACTGTAAACAAGACTATCTATTACCAATTCCTGAAGACAAAAT 624
QY 189 IleAsn 190
DB 625 GTCTCC 630

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/ TITLE OF INVENTION: ANTISENSE
/ TITLE OF INVENTION: Oligonucleotides Targeting Cooperating Oncogenes
/ NUMBER OF SEQUENCES: 55
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P. C.
/ STREET: Two Penn Center, Suite 1800
/ CITY: Philadelphia
/ STATE: Pennsylvania
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
/ COMPUTER: IBM PS/2
/ OPERATING SYSTEM: MS-DOS
/ SOFTWARE: WordPerfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/306,691B
/ FILING DATE: September 15, 1994
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 8321-8
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ TELEX: No. 5734039e
/ INFORMATION FOR SEQ ID NO: 45:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3225 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-08-306-691B-45

Alignment Scores:
Pred. No.: 3.13e-27 Length: 3225
Score: 305.50 Matches: 70
Percent Similarity: 59.34% Conservative: 38
Best Local Similarity: 38.46% Mismatches: 59
Query Match: 26.85% Indels: 15
DB: 1 Gaps: 7

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US-10-021-811-36 (1-206) x US-08-306-691B-45 (1-3225)

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QY 12 AEPProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleLeuMetAsnTyr 31
DB 372 AACCTGAGCTCATCAAGGCTCTTGGACCAAGAAAGATCAGAGTATAGAGCTT 431
QY 32 TLeaAaenHISGlyGluGlyValTTPAsnSerLeuAlaLysAlaGlyLeuLys-- 50
DB 432 GTACAGAAATTCAGGTCGAAACGTTGCTGTGTATTTGCCAAG-----CACTTAAAGGGG 485
QY 51 ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrLeuAsgProAspValArgArg 70
DB 486 AGAATTGGAAAACATGATGAGGAGAGGTCATTAACCACTTAATCCAGAGTTAAAGAAA 545
QY 71 GLyAenIleTrpProGluGluGlnLeuLeuIleMetGluLeuHISAlaLysTyrGlyAsn 90
DB 546 ACCTCTCGAGAGAGAGAGAGCAAGATTATTACCGACGACCAAGACGCTGGGAGAC 605
QY 91 ArgTyrSerLysIleAlaLysHISLeuProGlyArgThrAspAsnGluIleLysAsnTyr 110
DB 606 AGATGGGCAAGAAATCGCAAGAGCTAGCTGAGCAAGATGATATGCTATCCAGAACAC 665
QY 111 TrpArgThrArgIleGlnLysHISileLysGlnAlaGluAsnPhenGlnGlnSerSer 130
DB 666 TGGAAATTCACAAATGCGTCGGAAGGTGCAAG--GAAGGTATATCTGCAGAGTCTTCA 722
QY 131 AsnAsnSerGlu-----IleAsnAspHISGlnAlaSerThrSerHISValSerThrMet 148

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DB 723 AAGCCAGCCAGCCAGGAGGCGCCAGCAAGCTTCCAGAAAGACGATTTGATGGGTTTT 782
QY 149 AAGlupPrometGluMetYrSerProProCysTyrgIngluMetLeuGluPProPheSer 168
DB 783 GCTAG-----GCTCCGCTACAGCTCA-----CTCCCTGCCACT 818
QY 169 ThrGlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsn 188
DB 819 GGCAG---CCCACTGTATACAGCACTATTCCTATTACACATTTCTGAAGCAAAAT 875
QY 189 IleAsn 190
DB 876 GTCCTC 881
RESULT 6
PCT-US93-06251-91
; Sequence 91, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-06251-91
Alignment Scores:
Pred. No.: 3,13e-27 Length: 3225
Score: 305.50 Matches: 70
Percent Similarity: 59.34% Conservative: 38
Best Local Similarity: 38.46% Mismatches: 59
Query Match: 26.85% Indels: 15
DB: 5 Gaps: 7
US-10-021-811-36 (1-206) x PCT-US93-06251-91 (1-3225)
QY 12 AspProGluValArgIleGlyGlyProThrPheMetGluGluAspLeuIleLeuMetAsnTyr 31
DB 372 AACCTGAGCTCATCAGAGGCTCTTGACCAAGAAAGATCAAGAGGTATGAGCTT 431
QY 32 IleAlaAsnHisGlyGluGluIleValThrPheSerLeuAlaIleAlaGlyLeuLys--- 50
DB 432 GTACAGAAATACGCTCCGAAACGTTGCTGTATTGCGCAG-----CACTTAAGGGG 485

QY 51 ArgAsnGlyLysSerCysArgLeuArgTrpLeuAsnTyrIleAsnArgProAspValArgArg 70
DB 486 AGAATTGGAAACATATGAGGAGAGGTGGCATTAACCACTGAAATCCAGAGTTAAGAAA 545
QY 71 GlyAsnIleThrProGluGluGluLeuLeuIleMetGluMetIleAlaLysTrpGlyAsn 90
DB 546 ACCCTGTCGAGGAAGAGAGAGAGAGATTTATTAACAGGACACACAGACACTGGGGAGAC 605
QY 91 ArgTyrSerLysIleAlaLysHisLeuPProGlyArgThrAspAsnGluIleLysAsnTyr 110
DB 606 AGATGGCAGAAATGCAAGAGCTACTGCTGGACGAATGATATGATATCAAGAACAC 665
QY 111 TYPArgThrArgIleGluLysHisIleLysGlnAlaGluAsnPheGlnGlnSerSer 130
DB 666 TCGAATTTCAACAATGCTGCGAAGGTGCAACAG---GAAGGTATCTGACAGAGCTTCA 722
QY 131 AsnAsnSerGlu-----IleAsnAspHisGlnAlaSerThrSerHisValSerThrMet 148
DB 723 AAGCCAGCCAGCCAGCAAGCTTCCAGAAAGACGATTTGATGGGTTTT 782
QY 149 AAGlupPrometGluMetYrSerProProCysTyrgIngluMetLeuGluPProPheSer 168
DB 783 GCTAG-----GCTCCGCTACAGCTCA-----CTCCCTGCCACT 818
QY 169 ThrGlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsn 188
DB 819 GGCAG---CCCACTGTATACAGCACTATTCCTATTACACATTTCTGAAGCAAAAT 875
QY 189 IleAsn 190
DB 876 GTCCTC 881
RESULT 7
PCT-US93-06251-89
; Sequence 89, Application PC/TUS9306251
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric and Rife, Jason P.
; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06251
; FILING DATE: 19930630
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3230 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US93-06251-89

Alignment Scores:

Pred. No.: 3,14e-27 Length: 3230
 Score: 305.50 Matches: 70
 Percent Similarity: 59.34% Conservative: 38
 Best Local Similarity: 38.46% Mismatches: 59
 Query Match: 26.85% Indels: 15
 DB: 5 Gaps: 7

US-10-021-811-36 (1-206) x PCT-US93-06251-89 (1-3230)

QY 12 AspProGluValArgLysGlyProThrPheMetGluGluAspLeuLeuMetAsnTyr 31
 Db 262 AACCTGAGCTATCATAGGGTCTTGACCAAGAAAGATCGAGAGTATGAGCTT 321
 QY 32 TleAlaAsnHisGlyGluGlyValTyrAsnSerLeuAlaLysAlaGlyLeuLys--- 50
 Db 332 GTACGAAATACGCTCCGAAAGCTTGCTGTATTCGCAAG-----CACTAAAGGGG 375
 QY 51 ArgAsnGlyLysSerCysArgLeuArgTyrPleuAsnTyrLeuArgProAspValArgArg 70
 Db 376 AGAATTGGAAAAACAATGAGGAGGTGGCATTAACCACTTGAAATCCAGAGTTAAGAAA 435
 QY 71 GlyAsnIleThrProGluGluGlnLeuLeuMetGluLeuHisAlaLysTyrGlyAsn 90
 Db 436 ACCTCTGACGAAAGAGAAAGACAGAAATATTATTCACGCAACAGAGAGCTGGGAAAC 495
 QY 91 ArgTyrSerLysIleAlaLysHisIleuProGlyArgThrAspAsnGluLysAlaAsnTyr 110
 Db 496 AGATGGCAGAAATGCAAGAGTACTGCTGAGCAATGATTAATGCAATCAAGAACAC 555
 QY 111 ThrArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnSerSer 130
 Db 556 TGGAAATTCAATGCGTGGAGAGGTGCAACAG--GAAGGTATCTGCAAGAGCTTCA 612
 QY 131 AsnAsnSerGlu-----IleAsnAspHisGlnAlaSerThrSerHisValSerThrMet 148
 Db 613 AAAGCCAGCCAGCCAGGAGGCTCCAGAGCTTCCAGAAAGACATCTTATGAGGTTT 672
 QY 149 AlaGluProMetGluMetTyrSerProProCysTyrGlnGlyMetLeuGluProPheSer 168
 Db 673 GCTCAG-----GCTCCGCTTACAGCTCA-----CTCCCTGCCACT 708
 QY 169 ThrGlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsn 188
 Db 709 GGCCAG---CCCACTGTTAACAAGCATATCTTATTAACCATTTCTGAAGACAAAT 765
 QY 189 IleAsn 190
 Db 766 GTCCTC 771

RESULT 8

US-09-167-322-10

Sequence 10, Application US/09167322

Patent No. 6365151

GENERAL INFORMATION:

APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S.

England, James M.

TITLE OF INVENTION: CANCER VACCINE

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavoigna & Monaco, P.C.

STREET: Suite 1800, Two Penn Center Plaza

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/167,322

FILING DATE: 07-Oct-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/00582

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 7933-33 PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1897 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Alignment Scores:

Pred. No.: 2.04e-26 Length: 1897
 Score: 296.00 Matches: 73
 Percent Similarity: 53.47% Conservative: 35
 Best Local Similarity: 36.14% Mismatches: 55
 Query Match: 26.01% Indels: 40
 DB: 4 Gaps: 9

US-10-021-811-36 (1-206) x US-09-167-322-10 (1-1897)

QY 12 AspProGluValArgLysGlyProThrPheMetGluGluAspLeuLeuMetAsnTyr 31
 Db 233 AACCCAGAACTTAACAAGAGTCCATGACCTAAGAGAGAGATCAAGGTAAATAGAAC 292
 QY 32 TleAlaAsnHisGlyGluGlyValTyrAsnSerLeuAlaLysAlaGlyLeuLys--- 50
 Db 293 GTGCAAAATATGAGTCAAGAGCTGGAGCATTTGCTTAAG-----CAATTAAGGGA 346
 QY 51 ArgAsnGlyLysSerCysArgLeuArgTyrPleuAsnTyrLeuArgProAspValArgArg 70
 Db 347 AGATGGCAGAAATGCAAGAGTGGAGAGGTGGCAACACATCTGAATCCAGAGTGAAGAA 406
 QY 71 GlyAsnIleThrProGluGluGlnLeuLeuMetGluLeuHisAlaLysTyrGlyAsn 90
 Db 407 ACCTCTGACGAAAGAGGAGATGAAATTTATTAACGACACACAGAGACTGGGAAAC 466
 QY 91 ArgTyrSerLysIleAlaLysHisIleuProGlyArgThrAspAsnGluLysAlaAsnTyr 110
 Db 467 AGATGGCAGAAATGCAAGAGTGGAGAGGTGGCAACACATCTGAATCCAGAGTGAAGAA 526
 QY 111 ThrArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPheGlnGlnSerSer 130
 Db 527 TGAATTTCCACATCGCGCGGAAGGTGAGCAG--GAGGGTTACCCGAGAGTCTCC 583
 QY 131 Asn-----AsnSerGluIleAsnAspHisGlnAlaSerThrSerHisValSerThr 147
 Db 584 AAAGCCGCGCGCTGGCAACACCGGCTTCCAGAGAGC--AGCAATGATGAGCC 640
 QY 148 MetAlaGluProMetGluMetTyrSerProProCys----- 159
 Db 641 TTGGC-----CACACCCACCTGACAGGCCCGCGGGGGCGGCGAG 685
 QY 160 -----TyrGlnGlyMetLeuGluProPheSerTh----- 169
 Db 686 GCCCTCTGGGAGTACTACCCCTATTAACCAATTTGTCGCAAAATGTCCTGCT 745
 QY 170 GlnPhePro-----ThrIleAsnProAspGlnSerSerCys 181
 Db 746 CAGATCCCATATCCAGTAGCACTGATTAATATTATCAATTTCTCTCAACC-AGCTGC 804

QY 182 CysThr 183
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Db 805 TGCAGC 810

RESULT 9
US-09-402-929-5
/ Sequence 5, Application US/09402929
/ Patent No. 6410825
/ GENERAL INFORMATION:
/ APPLICANT: Temple University - Of The Commonwealth System of Higher Education
/ APPLICANT: Toscani, Antonio
/ APPLICANT: Hatton, Kimi
/ APPLICANT: Reddy, E. P.
/ TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
/ TITLE OF INVENTION: USES THEREOF
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
/ STREET: Suite 1800 Two Penn Center Plaza
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,929
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US98/06896
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 6056-214 PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4880 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-402-929-5

Alignment Scores:
Pred. No.: 26-25 Length: 4880
Score: 293.00 Matches: 70
Percent Similarity: 56.22% Conservative: 34
Best Local Similarity: 37.84% Mismatches: 57
Query Match: 25.75% Indels: 24
Gaps: 8

US-10-021-811-36 (1-206) x US-09-402-929-5 (1-4880)

QY 12 AspProGluValAlaGlySerGlyProTyrThrMetGluGluAspLeuIleLeuMetAsnTyr 31
Db 348 AATCCTGAATGATTAAGGCTCTTGACCTAAAGAAAGATCGAGGGTTATTGAATTA 407
QY 32 IleAlaAsnHisGlyGluGlyValTTPAsnSerLeuAlaIysAlaIaGlyLeuLys--- 50
Db 408 GTTACAGAAATATGAGCCCAAAAAGATGCTTTAATTGCAAAA-----CATTAAAAAGA 461
QY 51 ArgAsnGlyLysSerCysArgLeuArgTyrLeuAsnTyrLeuArgProAspValArg 70
Db 462 AGAATAGCAAGCACTGTAGAGAAAGATGCGATTAATCTCGAATCTCGAGGTAAAGAA 521
QY 71 GlyAsnIleThrProGluGluGlnLeuLeuIleMetGluLeuHisAlaLysTyrGlyAsn 90

Db 522 TCTTCCTGAGCAGAGAGAGCAGAGATCATATGAGACATTAAGCGGTGGAAAT 581
QY 91 ArgTyrSerIleAlaIysHisIleuProGluArgTyrAspAsnGluIleLysAsnTyr 110
Db 582 CGTTGGCAGAAATATGCGAACTACTTCAGAGAGCACTGATTAATTTCAAAAATAT 641
QY 111 TTPArgThrArgIleGlnLysHisIleLysGlnIaGluAsnPhenGlnGln-----Gln 128
Db 642 TGGAAATTCATCTAGCAAGAAAGATGAGACAGAGGGCTATTATTAAGAGGAAATAAA 701
QY 129 SerSerAsnAsnSerGluIleAsnAspHisGln-----AlaSerThrSerHisValSer 146
Db 702 TCAGACGATCTTCATCTTAACCTTCACACAAACCTTGCGAGCATATGATATGCA 761
QY 147 ThrMetAlaGluProMetGluMetTyrSerPro-----ProCysTyrGlnLysMet 163
Db 762 ACCAG-----AATCAGTTTACATACCTGTTCCAGATCCCTGGTATCAGATATG 812
QY 164 -----LeuGluProPheSerThr-----GlnPhePro 172
Db 813 TCACCTGAAGCAATGTATAGACATGTTCAGCTTCTGCTTTATTCAGCAACC 872
QY 173 ThrIleAsnProAsp 177
Db 873 TTCATTGATGAAGAT 887

RESULT 10
US-09-402-929-1
/ Sequence 1, Application US/09402929
/ Patent No. 6410825
/ GENERAL INFORMATION:
/ APPLICANT: Temple University - Of The Commonwealth System of Higher Education
/ APPLICANT: Toscani, Antonio
/ APPLICANT: Hatton, Kimi
/ APPLICANT: Reddy, E. P.
/ TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
/ NUMBER OF SEQUENCES: 7
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEIDEL, GONDA, LAVORGNA & MONACO, P.C.
/ STREET: Suite 1800 Two Penn Center Plaza
/ CITY: Philadelphia
/ STATE: PA
/ COUNTRY: U.S.A.
/ ZIP: 19102
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,929
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US98/06896
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Monaco, Daniel A.
/ REGISTRATION NUMBER: 30,480
/ REFERENCE/DOCKET NUMBER: 6056-214 PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-8383
/ TELEFAX: (215) 568-5549
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3602 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-09-402-929-1

Alignment Scores:
Pred. No.: 1,92e-25 Length: 3602
Score: 291.50 Matches: 64
Percent Similarity: 59.49% Conservative: 30
Best Local Similarity: 40.51% Mismatches: 51
Query Match: 25.62% Indels: 13
DB: 4 Gaps: 6

US-10-021-811-36 (1-206) x US-09-402-929-1 (1-3602)

QY 12 AspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleuMetAsnTyr 31
DB 500 AATCCGAATTATATAGAGGCTCTTGACTAAGAGAGATCAAGAGGTTATTAATTA 559
QY 32 IleAlaAsnHisGlyGluGlyValTTPaSerLeuAlaLysAlaGlyLeuLys--- 50
DB 560 GTTCCAGAAATATGGCCCAAAAAGGTGCTTTAATTGCAAAA-----CATTTAAAGGA 613
QY 51 ArgAsnGlyLysSerCysArgLeuArgTTPLeuAsnTyrLeuArgProAspValArgArg 70
DB 614 AATAATAGCGACAGTGCAGAGAAAGATGCGACATCACTGAACTTGAAGTGAAGAG 673
QY 71 GlyAsnIleThrProGluGluGluLeuIleMetGluLeuHisAlaLysTrpGlyAsn 90
DB 674 TCTTCTCGACAGAAAGAGAGACAGATCATATATGAAGCACACAGCGCTGGGAAC 733
QY 91 ArgTTPSerLysIleAlaLysHisLeuProGlyArgTTPAspAsnGluIleLysAsnTyr 110
DB 734 CTTGGGCGGAGATTCCTTAAGTACTTCTGAGAGACATGATTAATTCATAAATATCAT 793
QY 111 TTPArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPhcGln-----Gln 128
DB 794 TGGAAATTCACCATCGAAGAAAGTGAACAGAGGCTATTTCAGAGATGATATAAA 853
QY 129 SerSerAsnAsnSerGluIleAsnAspHisGln-----AlaSerThrSerHisValSer 146
DB 864 TCAGAGCGGCTCTTCATCAAAACTTCACACCAAACTTGTGGACATATGACCATTTGCA 913
QY 147 ThrMetAlaGluProMetGluMetCysTrpPro-----ProCysTyrGln 161
DB 914 ACCCAG-----AATCAGTTTATCATTTCTGTTCAAGATCCCTGGGTATCAG 958

RESULT 11
US-09-402-929-4
Sequence 4, Application US/09402929
Patent No. 6410825
GENERAL INFORMATION:
APPLICANT: Temple University - Of The Commonwealth System of Higher Education
APPLICANT: Toscani, Antonio
APPLICANT: Hatton, Kimi
APPLICANT: Reddy, E. P.
TITLE OF INVENTION: A-myb NULL MUTANT TRANSGENIC ANIMALS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, GONDA, LAVORGNA & MONACO, P. C.
STREET: Suite 1800 Two Penn Center Plaza
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,929
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/06896
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 6056-214 PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-5549
TELEFAX: (215) 568-8383
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-402-929-4

Alignment Scores:
Pred. No.: 5.01e-25 Length: 6775
Score: 291.50 Matches: 64
Percent Similarity: 59.49% Conservative: 30
Best Local Similarity: 40.51% Mismatches: 51
Query Match: 25.62% Indels: 13
DB: 4 Gaps: 6

US-10-021-811-36 (1-206) x US-09-402-929-4 (1-6775)

QY 12 AspProGluValArgLysGlyProTrpThrMetGluGluAspLeuIleuMetAsnTyr 31
DB 3749 AATCCGAATTATATAGAGGCTCTTGACTAAGAGAGATCAAGAGGTTATTAATTA 3808
QY 32 IleAlaAsnHisGlyGluGlyValTTPaSerLeuAlaLysAlaGlyLeuLys--- 50
DB 3809 GTTCCAGAAATATGGCCCAAAAAGGTGCTTTAATTGCAAAA-----CATTTAAAGGA 3862
QY 51 ArgAsnGlyLysSerCysArgLeuArgTTPLeuAsnTyrLeuArgProAspValArgArg 70
DB 3863 AGAATAGCGACAGTGCAGAGAAAGATGCGACATCACTGAACTTGAAGTGAAGAG 3922
QY 71 GlyAsnIleThrProGluGluGluLeuIleMetGluLeuHisAlaLysTrpGlyAsn 90
DB 3923 TCTTCTCGACAGAAAGAGAGACAGATCATATATGAAGCACACAGCGCTGGGAAC 3982
QY 91 ArgTTPSerLysIleAlaLysHisLeuProGlyArgTTPAspAsnGluIleLysAsnTyr 110
DB 3983 CGTTGGCGGAGATTCCTTAAGTACTTCTGAGAGACATGATTAATTCATAAATATCAT 4042
QY 111 TTPArgThrArgIleGlnLysHisIleLysGlnAlaGluAsnPhcGln-----Gln 128
DB 4043 TGGAAATTCACCATCGAAGAAAGTGAACAGAGGCTATTTCAGAGATGATATAAA 4102
QY 129 SerSerAsnAsnSerGluIleAsnAspHisGln-----AlaSerThrSerHisValSer 146
DB 4103 TCAGAGCGGCTCTTCATCAAAACTTCACACCAAACTTGTGGACATATGACCATTTGCA 4162
QY 147 ThrMetAlaGluProMetGluMetCysTrpPro-----ProCysTyrGln 161
DB 4163 ACCCAG-----AATCAGTTTATCATTTCTGTTCAAGATCCCTGGGTATCAG 4207

RESULT 12
US-08-306-691B-46
Sequence 46, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
APPLICANT: Skorek, Tomasz
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P. C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.

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; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,691B
; FILING DATE: September 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5549
; TELETYPE: No. 5734039e
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2638 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-306-691B-46

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Alignment Scores:
Pred. No.: 3.37e-23 Length: 2638
Score: 271.50 Matches: 67
Percent Similarity: 52.17% Conservative: 29
Best Local Similarity: 36.41% Mismatches: 59
Query Match: 23.86% Indels: 29
DB: 1 Gaps: 8

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US-10-021-811-36 (1-206) x US-08-306-691B-46 (1-2638)

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Qy 5 GlnGlnCysLys-----ThSerGlnAAsProGluValArgLysGluProTir 20
Db 326 CAGCATATCCACAGAGTGGCTGAGATCTTGTGATCCAGCTTGTGCAGGGCCATGG 385
Qy 21 ThrMetGluGluAspLeuIleuMetAsnTyrlleAlaAsnHisGlyGluGlyValTir 40
Db 386 ACCAAGAGGAGAGCCAAAGATCATGAGCTGTTAAGAGTATGCGACAAACAGCTGG 445
Qy 41 AsnSerIeuAlaLysAlaAlaGlyLeuLys--ArgAsnGlyLysSerCysArgLeuArg 59
Db 446 ACACTGATTGCCAAG-----CACCTGAAGGGCGGCTGGGGAAGCAGTGCCTGAACGC 499
Qy 60 TrpLeuAsnTyrlleuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 79
Db 500 TGGCAACAACCTTCAACCTGAGGTGAAGAGCTTGTGCTGAGCCGAGAGAGAGACCGC 559
Qy 80 LeuIleMetGluLeuHisAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHisIleu 99
Db 560 ATCATCTCGAGAGGCCCAAGAGTCTGGCAACCCCTGGCCGAGATGCCAAGATGTTG 619
Qy 100 ProGlyArgThrAspAsnGluIleLysAsnTyrlleArgGlyThrArgGlyGlnLysHisIle 119
Db 620 CCAGGAGAGAGAGCAATGCTGTGTAAGATCATGGAATCTACATCAAAAGAGAGTGT 679
Qy 120 LysGlnAlaGluAsnPhnGlnGlnInSerSerAsnAsnSer----- 133
Db 680 ---GACACAGAGAGCTTTTGAAGCGATGCAAGAGTCCAAAGCCCAAGTACTTGGCTG 736
Qy 134 ---GluIleAsnAspHisGlnAlaSerThrSerHisValSerThrMetAlaGluProMet 152
Db 737 CTGAGAGCTCGAGAGCAAGAGAGCGCTCCAGAGT-----GCCAGCCCAAG 781
Qy 153 GluMetTyrlSerProProCysTyrlGlnGlyMetLeuGluProPheSerThrGlnPhePro 172

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Db 782 GAA-----GCCACGAGGAAGTCTT-----CTGACCAACTGGGCC 814
Qy 173 ThrIleAsnPro 176
Db 815 TCCGTCCCTCCT 826

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RESULT 13
US-08-485-139-1
; Sequence 1, Application US/08485139
; Patent No. 5880331
; GENERAL INFORMATION:
; APPLICANT: KREBBERS, Emno
; APPLICANT: WILLIAMS, Mark
; TITLE OF INVENTION: USE OF ANTHOCYANIN GENES TO MAINTAIN
; TITLE OF INVENTION: MALE STERILE PLANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,139
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-2020
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: C1 gene of Zea mays
; FEATURE:
; NAME/KEY: -
; LOCATION: 279..284
; OTHER INFORMATION: /label= HpaI
; FEATURE:
; NAME/KEY: -
; LOCATION: 447..452
; OTHER INFORMATION: /label= EcoRI
; FEATURE:
; NAME/KEY: -
; LOCATION: 1735..1740
; OTHER INFORMATION: /label= AacII
; FEATURE:
; NAME/KEY: -
; LOCATION: 1505..1510
; OTHER INFORMATION: /label= EcoRI
; FEATURE:
; NAME/KEY: -
; LOCATION: 2081..2086
; OTHER INFORMATION: /label= XhoI
; FEATURE:
; NAME/KEY: -
; LOCATION: 2418..2430
; OTHER INFORMATION: /label= SfiI

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LOCATION: 447..452
OTHER INFORMATION: /label= EcORI
FEATURE:
NAME/KEY: -
LOCATION: 1735..1740
OTHER INFORMATION: /label= AatII
FEATURE:
NAME/KEY: -
LOCATION: 1505..1510
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OTHER INFORMATION: /label= XhoI
FEATURE:
NAME/KEY: -
LOCATION: 2418..2430
OTHER INFORMATION: /label= SfiI
FEATURE:
NAME/KEY: -
LOCATION: 2669..2674
OTHER INFORMATION: /label= SnaBI
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NAME/KEY: -
LOCATION: 2634..2639
OTHER INFORMATION: /label= SnaBI
FEATURE:
NAME/KEY: -
LOCATION: 3008..3013
OTHER INFORMATION: /label= HpaI
FEATURE:
NAME/KEY: -
LOCATION: 1..1077
OTHER INFORMATION: /label= Pci
OTHER INFORMATION: /note= "region containing promoter of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 1078..2134
OTHER INFORMATION: /label= C1
OTHER INFORMATION: /note= "coding region of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 2135..2430
OTHER INFORMATION: /label= 3'C1
OTHER INFORMATION: /note= "region containing polyadenylation signal of C1 gene"
FEATURE:
NAME/KEY: -
LOCATION: 1033..1038
OTHER INFORMATION: /label= TATA-Box
FEATURE:
NAME/KEY: -
LOCATION: 1061..1062
OTHER INFORMATION: /label= transcript-init
OTHER INFORMATION: /note= "transcription initiation site"
FEATURE:
NAME/KEY: intron
LOCATION: 1211..1299
FEATURE:
NAME/KEY: intron
LOCATION: 1430..1575
FEATURE:
NAME/KEY: -
LOCATION: 935..939
OTHER INFORMATION: /label= C1-S
OTHER INFORMATION: /note= "TGCAG sequence (in C1 gene) which in the C1-S sequence
OTHER INFORMATION: is changed to TTAGG"
US-08-750-357-1

Alignment Scores:
Pred. No.: 4.83e-20 Length: 4059
Score: 248.00 Matches: 62
Percent Similarity: 41.67% Conservative: 13
Best Local Similarity: 34.44% Mismatches: 26

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[illegible]

Search completed: February 8, 2003, 12:30:35
Job time : 55 secs

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;
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4824 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: plasmid pCOL9
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 396..401
;   OTHER INFORMATION: /label= EcoRI
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 2367..2379
;   OTHER INFORMATION: /label= SfiI
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 884..888
;   OTHER INFORMATION: /label= Cl-S
; OTHER INFORMATION: /note="TGCAG (in C1) which in Cl-S allele is
; OTHER INFORMATION: replaced with TTAG"
; US-08-485-139-5

Alignment Scores:
Pred. No.: 6.35e-20 Length: 4824
Score: 248.00 Matches: 62
Percent Similarity: 41.67% Conservative: 13
Best Local Similarity: 34.44% Mismatches: 26
Query Match: 21.79% Indels: 81
DB: Gaps: 2

US-10-021-811-36 (1-206) x US-08-485-139-5 (1-4824)

Oy 15 ValArgLysGlyProThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsn 34
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1060 GTTAAGAGAGGGCGCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 1119

Oy 35 HisGlyGluGlyValTyrAsnSerLeuAlaLys----- 45
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1120 CATGCGAAGGCAATGAGAGGAAAGT-GCCCCAGAAAGCCGTAATACTAGTCTTT 1178

Oy 45 ----- 45
Db 1179 TTATTTCATTTGGGATCATATATATACCCCGAGGCAAGACCGAGAGACGATCAGTGT 1238

Oy 46 --AlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTyrPleuAsnTyrLeu 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1239 GTGGGTGAGAGTTGCGTGGCGGCAAGAGCTGCCGGCTGGGCTGAACTACCTTC 1298

Oy 65 ArgProAspValArgArgGlyAsnIleThrProGluGluGluLeuIleMetGluLeu 84
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1299 CGGCCCAACATCAGCGCGGCAACTTCTCTTACGACGAGAGATCTCATCATCGGCTTC 1358

Oy 84 ----- 84
Db 1359 CACAGGCTCTCGGCAAGAGTGTGCGAGTGCACAGTGTGGCTAGCTTATTACAGA 1418

Oy 84 ----- 84
Db 1419 GCTGACGACGAGGCGATCGATCGAGCGTCTGCGAATTCTGTTCCGGTGTGGGCC 1478

Oy 85 -----HisAlaLysTyrGlyAsnArgTyrPserLysIle 95
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1479 GTGGAGAGTAGCTCATTCATATGTATCATGCTGTTGGCG-CGACAGTGTGCTGATT 1537

Oy 96 AlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTyrPargThrArgIle 115
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1538 GTAAGCAGGCTGCTGCGCCGACACACATATCAAGAACTAGTAACAGCAGCGCTG 1597
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 8, 2003, 11:08:55 ; Search time 60 Seconds
(without alignments)
1627.410 Million cell updates/sec

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1138
Sequence: 1 MDKQCKTSDPEVRKGPW.....NNINYSMEDSWMQLINGD 206

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 408267 seqs, 237001491 residues

Total number of hits satisfying chosen parameters: 816534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-MAXLEN=200000000 -USER=US10021811@cgn 1.1.33 @runac 03022003 11222 25671
-NCPU=6 -ICPU=3 -NO XLPXY -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAEXT=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1138	100.0	863	9	US-10-021-811-35
2	1062	93.3	988	9	US-10-021-811-29
3	874.5	76.8	805	9	US-10-021-811-37
4	829.5	72.9	910	9	US-10-021-811-33

5	609	53.5	382	10	US-09-878-574-1305	Sequence 1305, Ap
6	591	51.9	530	9	US-10-021-811-31	Sequence 31, Appl
7	587.5	51.6	392	10	US-09-878-574-33	Sequence 33, Appl
8	586	51.5	438	10	US-09-878-574-5021	Sequence 5021, Ap
9	562	49.4	375	10	US-09-878-574-327	Sequence 327, App
10	560.5	49.3	379	10	US-09-878-574-3147	Sequence 3147, Ap
11	556.5	48.9	350	10	US-09-878-574-50	Sequence 50, Appl
12	545.5	47.9	365	10	US-09-878-574-194	Sequence 194, App
13	528	46.4	1236	9	US-10-021-811-45	Sequence 45, Appl
14	519.5	45.7	587	9	US-10-021-811-17	Sequence 17, Appl
15	518.5	45.6	1181	9	US-10-021-811-47	Sequence 47, Appl
16	508.5	44.7	1317	9	US-10-021-811-9	Sequence 9, Appl
17	505	44.4	500	9	US-10-021-811-41	Sequence 41, Appl
18	503.5	44.2	1348	9	US-10-021-811-43	Sequence 43, Appl
19	502.5	44.2	557	9	US-10-021-811-27	Sequence 27, Appl
20	494.5	43.5	352	10	US-09-878-574-2390	Sequence 2390, Ap
21	494	43.4	771	9	US-10-021-811-1	Sequence 1, Appl
22	490	43.1	1186	9	US-10-021-811-49	Sequence 49, Appl
23	485	42.6	751	9	US-10-021-811-39	Sequence 39, Appl
24	475	41.7	822	9	US-09-938-842A-2373	Sequence 2373, Ap
25	464	40.8	786	9	US-09-938-842A-2294	Sequence 2294, Ap
26	459	40.3	810	9	US-09-938-842A-1293	Sequence 1293, Ap
27	447	39.3	640	9	US-10-021-811-21	Sequence 21, Appl
28	438	38.5	521	9	US-10-021-811-59	Sequence 59, Appl
29	419	36.8	708	9	US-09-938-842A-1292	Sequence 1292, Ap
30	418.5	36.8	293	10	US-09-878-574-2675	Sequence 2675, Ap
31	415.5	36.5	771	9	US-09-938-842A-2242	Sequence 2242, Ap
32	410	36.0	960	9	US-09-938-842A-2138	Sequence 2138, Ap
33	400.5	35.2	774	9	US-09-938-842A-2636	Sequence 2636, Ap
34	394	34.6	782	9	US-10-021-811-3	Sequence 3, Appl
35	393.5	34.6	1123	9	US-10-021-811-13	Sequence 13, Appl
36	391	34.4	514	9	US-10-008-118A-5	Sequence 5, Appl
37	391	34.4	514	10	US-09-443-704-5	Sequence 5, Appl
38	390.5	34.3	741	9	US-09-938-842A-121	Sequence 121, Appl
39	387.5	34.1	601	9	US-10-021-811-5	Sequence 5, Appl
40	387	34.0	1141	9	US-10-008-118A-11	Sequence 11, Appl
41	387	34.0	1141	10	US-09-443-704-11	Sequence 11, Appl
42	385	33.8	849	9	US-09-938-842A-2082	Sequence 2082, Ap
43	384	33.7	1168	9	US-10-008-118A-23	Sequence 23, Appl
44	384	33.7	1168	10	US-09-443-704-23	Sequence 23, Appl
45	382.5	33.6	1044	10	US-09-770-445-167	Sequence 167, Appl

ALIGNMENTS

RESULT 1
US-10-021-811-35
Sequence 35, Application US/10021811
Publication No. US20030024007A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: B01294 US NA
CURRENT APPLICATION NUMBER: US/10/021, 811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 35
LENGTH: 863
TYPE: DNA
ORGANISM: Glycine max
US-10-021-811-35

Alignment Scores:
Pred. No.: 4.9e-127 Length: 863
Score: 1138.00 Matches: 206
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-021-811-36 (1-206) x US-10-021-811-35 (1-863)

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QY 1 MetApLySLySGInGInCysLySThrSerGInAspProGluValArgLySGlyProTyr 20
DB 29 ATGGATTAAAAACAACTGTGAAGCGTCTCAAGATCCTGAAGTGAAGAAAGGAGGCTTTGG 88
QY 21 ThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHISGlyGluValTyr 40
DB 89 ACATATGGAAGAAAGACTTGTATCTGATGAATATATTGCAATATCAGGGGAAGGTGTTGG 148
QY 41 AmsSerLeuAlaLySAIAlaGlyLeuLySAArgAsnGlyLySerCysArgLeuArgTyr 60
DB 149 AACTCTTTGGCCAAAGCTGTGCTGTCTCAACGTAAAGGAAAGAGTTGCCGCTAAGGTGG 208
QY 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
DB 209 CTAAATTACTCTCCGTCTGATGTTAGAAGAGGAATATTACACCCGAGAAACAATTG 268
QY 81 IleMetGluLeuHISAlaLySThrGlyAsnArgTyrSerIleAlaLySHISLeuPro 100
DB 269 AATTATGGAGCTTCACGCAAGGGGAAACAGGTGTCTCAAAATTTGCCAGCATCTAACC 328
QY 101 GlyArgThrAspAsnGluIleLyAsnTyrTyrArgThrArgIleGlnLySHISLeu 120
DB 329 GAAAGAGCTGATTAATGATCAAGAACTATTGAGAGCAAGATCCAGAAAGCATCATCAG 388
QY 121 GAlaGluAsnPhenGlnGlnSerSerAsnSerGluIleAsnAspHISGlnAla 140
DB 389 CAAAGTGAACTTTCACCAACAGAGTATATATTTGTGATTAATATGATCACCAAGCT 448
QY 141 SerThrSerHISValSerThrMetAlaGluProMetGluMetTyrSerProCysTyr 160
DB 449 AGCACTACCAATGTTTCCACCATGGCTGAGCCCATGAGAGATGATTTCTCCACCTGTTAT 508
QY 161 GlnGlyMetLeuGluProPhenSerThrGlnPheProThrIleAsnProAspGlnSer 180
DB 509 CAAAGAAATGTGAAGCCATTTCACATCACTGATCCCTACAAATTAATCCGATCAATCCAG 568
QY 181 CysCysThrAsnAspAsnAsnAsnIleAsnTyrTyrSerMetGluAspSerTyrSerMet 200
DB 569 TGTGTATACCAATGACAAACAACAACATTAACTATTGACATGAGAGATAGCTGTGATG 628
QY 201 GlnLeuLeuAsnGlyAsp 206
DB 629 CAATTACTGAACGGTGAT 646
```

RESULT 2

US-10-021-811-29
; Sequence 29, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Ode11, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BB1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021.811
; PRIORITY FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 29
; LENGTH: 988
; TYPE: DNA
; ORGANISM: Glycine max
US-10-021-811-29

Alignment Scores:

Pred. No.: 7,44e-118 Length: 988
Score: 1062.00 Matches: 197
Percent Similarity: 95.67% Conservative: 2
Best Local Similarity: 94.71% Mismatches: 7
Query Match: 93.32% Indels: 2
DB: 9 Gaps: 2

US-10-021-811-36 (1-206) x US-10-021-811-29 (1-988)

```
QY 1 MetApLySLySGInGInCysLySThrSerGInAspProGluValArgLySGlyProTyr 20
DB 61 ATGGATTAAAAACAACTGTGAAGCGTCTCAAGATCCTGAAGTGAAGAAAGGAGGCTTTGG 120
QY 21 ThrMetGluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHISGlyGluValTyr 40
DB 121 ACGATGGAAGAAAGACTTGTATCTGATGAATATATTGCAATATCAGGGGAAGGTGTTGG 180
QY 41 AmsSerLeuAlaLySAIAlaGlyLeuLySAArgAsnGlyLySerCysArgLeuArgTyr 60
DB 181 AATTCTTTGGCCAAAGCTGTGCTGTCTCAACGTACCGGAAAGAGTTGCCGCTAAGGTGG 240
QY 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
DB 241 CTAAATTACTCTCCGTCTGATGTTAGAAGAGGAATATTACACCCGAGAAACAATTG 300
QY 81 IleMetGluLeuHISAlaLySThrGlyAsnArgTyrSerIleAlaLySHISLeuPro 100
DB 301 ATCATGAGAGCTTCACGCAAGGGGAAACAGGTGTCTCAAAATTTGCCAGCATCTAACC 360
QY 101 GlyArgThrAspAsnGluIleLyAsnTyrTyrArgThrArgIleGlnLySHISLeu 120
DB 361 GGTAGACAGATTAATGATCAAGAACTATTGAGAGCAAGATCCAGAAAGCATCATCAG 420
QY 121 GAlaGluAsnPhenGlnGlnSerSerAsnSerGluIleAsnAspHISGlnAla 140
DB 421 CAAAGTGAACTTTCACCAACAGAGTATATATTTGTGATTAATATGATCACCAAGCT 480
QY 141 SerThrSerHISValSerThrMetAlaGluProMetGluMetTyrSerProCysTyr 160
DB 481 AGCACTACCAATGTTTCCACCATGGCTGAGCCCATGAGAGATGATTTCTCCACCTGTTAT 540
QY 161 GlnGlyMetLeuGluProPhenSerThr---GlnPheProThrIleAsnProAspGlnSer 179
DB 541 CAAAGAAATGTGAAGCCATTTCACATCACTGATCCCTACAAATTAATCCGATCAATCCAG 600
QY 180 SerCysCysThrAsnAspAsnAsn---IleAsnTyrTyrSerMetGluAspSerTyr 198
DB 601 AGTTGTTGACCAATGACAAACAACAACATTAACTATTGAGCATGAGAGATATCTGG 660
QY 199 SerMetGlnLeuLeuAsnGlyAsp 206
DB 661 TCATATCAGTTACTGAACGGGGAT 684
```

RESULT 3

US-10-021-811-37
; Sequence 37, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Ode11, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BB1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021.811
; PRIORITY FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 37
; LENGTH: 805
; TYPE: DNA

```
; ORGANISM: Glycine max
US-10-021-811-37

Alignment Scores:
Pred. No.: 1,51e-95      Length: 805
Score: 874.50           Matches: 168
Percent Similarity: 85.51%  Conservative: 9
Best Local Similarity: 81.16%  Mismatches: 23
Query Match: 76.85%      Indels: 7
DB: Gaps: 5

US-10-021-811-36 (1-206) x US-10-021-811-37 (1-805)

Qy 4 LysGlnGlnCys---LysThrSerGlnAspProGluValArgLysGlyProTyrThrMet 22
   |||::|
Db 1 AAAAAACCATGCACTCATCTCATGATCTCTGAAGTGAAGAAAGGACCATGACCATG 60

Qy 23 GluGluAspLeuIleLeuMetCysTyrIleAlaAsnHsGlyGluGlyValTyrPasnSer 42
   |||::|
Db 61 GAGAGAGACTGATCTGATTAACCTATATTGCAATATCAACGATGAAGGTTGTTGAACTCC 120

Qy 43 LeuAlaLysAlaIleGlyLeuLysArgAsnGlyLysSerCysArgLeuAryTyrPasn 62
   |||::|
Db 121 TTAGCCAAAGCTTCTGCTGCTCAACGAAACGAGAGATTGTCATCCGTTGCTAAAC 180

Qy 63 TyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuIleMet 82
   |||::|
Db 181 TACCTTCCTCTGATGTTTGAAGAAGAAACATTACACCCGAGAAACAGCTTTTATCATATA 240

Qy 83 GluLeuHsAlaLysTyrPgiLysAsnArgTyrPserLysIleAlaLysHsIleuProGlyArg 102
   |||::|
Db 241 GAACCTTCATGCAAGTGGGCAATAGTGGTCCAAAATTGCAAAAGCATCTTCCAGGAAGA 300

Qy 103 ThrAspAsnGluIleLysAsnTyrTyrArgThrArgIleGlnLysHsIleLysGlnAla 122
   |||::|
Db 301 ACTGCAATGAGATTAAACATCTCTGAGAACAGAGATCCAAAAGCACAATTAAGCAAGCT 360

Qy 123 GluAsnPhenGlnGlnSerSerAsnAsnSerGluIleAsnAspHsIleGlnAla----- 140
   |||::|
Db 361 GAGACTTCACAAACAAACAT-----GCTAATTCAAGAAATATGATCATCAAGCAAGCACT 414

Qy 141 SerThrSerHsIleValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyr 160
   |||::|
Db 415 AGTACTACCAAGATGTCACCATGATGCAATCAATGAGCACTTCTCTCCACCTCATAC 474

Qy 161 GlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsnProAspGlnSerSer 180
   |||::|
Db 475 CAAGGAACCTTTGAGCCATTCACACTCAATTCCTCTACAAATCACT--GATCAATCAAGT 531

Qy 181 CysCysThrAsnAspAsnAsnAsnIleAsnTyrTyrPserMetGluAspSerTyr---Ser 199
   |||::|
Db 532 TGTTTTACCAACCAACCAAGCAACAACTATTGAGACATCGAGATATATGATCGTCT 591

Qy 200 MetGlnLeuLeuAsnGlyAsp 206
   |||::|
Db 592 ATGCAATTACTCAATGAGAT 612

RESULT 4
US-10-021-811-33
; Sequence 33, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odell, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BB1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
```

```
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (798)
; NAME/KEY: unsure
; LOCATION: (807)
; NAME/KEY: unsure
; LOCATION: (814)
US-10-021-811-33

Alignment Scores:
Pred. No.: 4.38e-90      Length: 910
Score: 829.50           Matches: 168
Percent Similarity: 83.89%  Conservative: 9
Best Local Similarity: 79.62%  Mismatches: 23
Query Match: 72.89%      Indels: 12
DB: Gaps: 7

US-10-021-811-36 (1-206) x US-10-021-811-33 (1-910)

Qy 1 MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTyr 20
   |||::|
Db 37 ATGACCAAAAA---CATGCGACTCATCTCATGATCCAGAAAGTGAAGGACCATGCG 93

Qy 21 ThrMetGluGluAspLeuIleLeuMetCysTyrIleAlaAsnHsGlyGluGlyValTyr 40
   |||::|
Db 94 ATCATGAAAGAAAGACTGATCTTGATTAACCTATATTGCAAAATCAACGATGAAGTGTGG 153

Qy 41 AsnSerLeuAlaLysAlaIleGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTyr 60
   |||::|
Db 154 AATCTTTAGCCAAAGCTTCTGCTCTTAAGCAACGAGAAAGATTGTCATCCGTTGG 213

Qy 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
   |||::|
Db 214 CTAACTACCTTCGCTCTGATGTTAGAAAGAGAAACATTACCCGAAAGAACAGCTTTTG 273

Qy 81 IleMetGluLeuHsAlaLysTyrPgiLysAsnArgTyrPserLysIleAlaLysHsIleuPro 100
   |||::|
Db 274 ATATGAACTTCATCAAGTGGGCAATAGGTGCTCAAAATTGCAAGCATCTTCCA 333

Qy 101 GlyArgThrAspAsnGluIleLysAsnTyrTyrArgThrArgIleGlnLysHsIleLys 120
   |||::|
Db 334 GGAAGAATCGACATGATGATTAAGAACTCTGGAAGACTAGATCCAGAACCATTAAG 393

Qy 121 GlnAlaGluAsnPhenGlnGln-----GlnSerSerAsnAsnSerGluIleAsnAspHs 138
   |||::|
Db 394 CAAGCTGAGACTTCACAAACAACTGTAAATTCATCAGAGAAATAGTAAT--AATGATCAT 450

Qy 139 GlnAla-----SerThrSerHsIleValSerThrMetAlaGluProMetGluMetTyrSer 156
   |||::|
Db 451 CAAGCAAGCAATAGCACTGACCAAGGTGTCACATGCAATGCAATCAATGACTTCTCT 510

Qy 157 ProProCysTyrGlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsnPro 176
   |||::|
Db 511 TCACCTCATACCAACCAACTTTTGAAGCATTTCA-ACCTCAATTCCTCAATCAAT--- 566

Qy 177 AspGlnSerSerCysCysThrAsnAspAsnAsnIleAsnTyrTyrPserMetGluAsp 196
   |||::|
Db 567 GATCAATCAAGATTGTTGTCACGCAACAAAC-----AATATTGAGCATCGAGAT 617

Qy 197 SerTyr---SerMetGlnLeuLeuAsnGlyAsp 206
   |||::|
Db 618 ATCTGTCTCTATGCAATTACTCAATGAGAT 650

RESULT 5
US-09-878-574-1305
; Sequence 1305, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO: 1305
; LENGTH: 382
; TYPE: RNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB028-039-Q1-B1-G9
US-09-878-574-1305

Alignment Scores:
Pred. No.: 2,96e-64 Length: 382
Score: 609.00 Matches: 110
Percent Similarity: 93.60% Conservative: 7
Best Local Similarity: 88.00% Mismatches: 8
Query Match: 53.51% Indels: 0
DB: 10 Gaps: 0

US-10-021-811-36 (1-206) x US-09-878-574-1305 (1-382)

QY 10 SerGlnAAPPProGluValArgLysGlyProThrPhrMetGluGluValAspLeuMet 29
Db 2 TCTCATGATCCGAAAGTACAGGAGGAGGACCATGATCATGAGAGGAGCATTTGATTTATA 61
QY 30 AsnTyrTllealaAsnHsGlyGluGlyValTrrpAsnSerleuAlaLysAlaGlyLeu 49
Db 62 AACATATTTGCAATTCACGGTGAAGGTGTGGAATTCCTTACGCAAGCTTCGTGCTT 121
QY 50 LysArgAsnGlyLysSerCyArgLeuArgTrrpLeuAsnTyrLeuAspProAspValArg 69
Db 122 AAAGGAAAGCGGAAAGAGTGTGCGACTCCGTTGGCTTAACTTCTTCCTGATTTAGA 181
QY 70 ArgGlyAsnTlleThrProGluGluGlnLeuLeuTleMetGluLeuHsAlaLysTrrpGly 89
Db 182 AAGAGAAACATTACACCCGAGAGACACCTTTGATCATAGAACTTCATGCAAAAGTGGGCG 241
QY 90 AsnArgTrrpSerLysLleAlaLysHsLysLeuProGlyArgTrrpAsnGluTlleLysAsn 109
Db 242 AATAGGTGTGTCAAATTTGCAAGACATCTTCAGGAGAGACTGACATGAGATTAGAAC 301
QY 110 TyrTrrpArgThrArgTlleGlnLysHsLleLysGlnAlaGluAsnPhgGlnGlnSer 129
Db 302 TTCTGGAAACTAGGATTCAGAAACACATTAAAGCAAGCTTGACAAACAACATGGT 361
QY 130 SerAsnAsnSerGlu 134
Db 362 AATTCATCCAGAGA 376

RESULT 6
US-10-021-811-31
; Sequence 31, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwon
; APPLICANT: Odell, Joan
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: BB1294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
```

```

; SEQ ID NO 31
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (301)
; NAME/KEY: unsure
; LOCATION: (356)
; NAME/KEY: unsure
; LOCATION: (388)
; NAME/KEY: unsure
; LOCATION: (393)
; NAME/KEY: unsure
; LOCATION: (470)
; NAME/KEY: unsure
; LOCATION: (485)
; NAME/KEY: unsure
; LOCATION: (495)
; NAME/KEY: unsure
; LOCATION: (513)
; NAME/KEY: unsure
; LOCATION: (517)
; NAME/KEY: unsure
; LOCATION: (522)
US-10-021-811-31

Alignment Scores:
Pred. No.: 6.84e-62 Length: 530
Score: 591.00 Matches: 122
Percent Similarity: 83.33% Conservative: 8
Best Local Similarity: 78.21% Mismatches: 25
Query Match: 51.93% Indels: 3
DB: 9 Gaps: 1

US-10-021-811-36 (1-206) x US-10-021-811-31 (1-530)

QY 1 MetAspLysLysGlnGlnCysLysThrSerGlnAAPPProGluValArgLysGlyProTrrp 20
Db 7 ATGGACAAGAGAGCTTGGGCG--AACACGTCTCATGATCTCGAAGGAGAGGCGGCATGG 63
QY 21 ThrMetGluGluAAPPLeuTlleMetAsnTyrTlleAlaAsnHsGlyGluGlyValTrrp 40
Db 64 ACAATGGAAGAAAGCTTATATCTGATCATCTATATTCGCATTCACGGGAAAGGGGTTGG 123
QY 41 AsnSerLleuAlaLysAlaGlyLysLeuLysArgAsnGlyLysSerCyArgLeuArgTrrp 60
Db 124 AACTCTTTGGCCCAAGGCTGCTGGACTTAAACGTACCGGAAAGAGTTCCCGCTCCGGTGG 183
QY 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnTlleThrProGluGluGlnLeu 80
Db 184 CTAAACTACTCCCGTCCGTGATGTTTGAAGAGGAGATTTTACACCCGAGAACAGCTTTTG 243
QY 81 TleMetGluLeuHsAlaLysTrrpGlyAsnArgTrrpSerLysLleAlaLysLysLeuPro 100
Db 244 ATCATGGAACCTTCATGCAAGAGTGGGAAACAGGTGTCCAAATTTGCCAAGCATCTTACC 303
QY 101 GlyArgThrAspAsnGluTlleLysAsnTyrTrrpArgThrArgTlleGlnLysHsLleLys 120
Db 304 GGAAGGACTGATTAATGAGATTAGAACTACTGAGGAGCAAGAT--CAAGAAACANCTCAG 362
QY 121 GlnAlaGluAsnPhgGlnGlnSerSerAsnAsnSerGluTlleAsnPhsGlnAla 140
Db 363 CAAAGCTTCACACAA--CTTCACACACANAGTANTTATTTGATATTTTACATCCCAAGC 421
QY 141 SerThrSerHsValSerThrMetAlaGluProMetGluMetTyrSer 156
Db 422 TTGCACAACCAATTTGTCACATGCGCAACCCAAAAAACCTAATCTCA 469

RESULT 7
US-09-878-574-33
; Sequence 33, Application US/09878574
; Patent No. US20020110548A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 33
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-A8
; US-09-878-574-33

Alignment Scores:
Pred. No.: 1,156-61 Length: 392
Score: 587.50 Matches: 109
Percent Similarity: 91.80% Conservative: 3
Best Local Similarity: 89.34% Mismatches: 9
Query Match: 51.63% Indels: 1
DB: 10 Gaps: 1

US-10-021-811-36 (1-206) x US-09-878-574-33 (1-392)
Qy 1 MetAspLySgInGInCysLySThrSerGlnAspProGluValArgLySgLyProTr 20
Db 29 ATGACAAAGAAAGCTTGCG--AACACGCTCATGATCTCGAAGTGAAGAAAGGCGCATGG 85
Qy 21 ThrMetGluGluAspLeuIleLeuMetAsnTyrlleAlaAsnHisgLyGluGlyValTr 40
Db 86 ACAATGGAAGAAAGCTTATCTTGATCACTATATTTGCCAATTCACGGGGAAGGGGATTGG 145
Qy 41 AsnSerLeuAlaLySAlaAlaGlyLeuLySArgAsnGlyLySArgCysArgLeuArgTr 60
Db 146 AACTTTTGGCCAAAGCTGCTGGACTTAACGTAACCGGAAGAGTTGGCGGCTCGGTTGG 205
Qy 61 LeuAsnTyrlLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
Db 206 CTAACACTACCTCCGCTCGTGAATTTAGAAAGAGGAATATTACACCGAAGCAAGCTTTTG 265
Qy 81 IleMetGluLeuHisAlaLySArgGlyAsnArgTrpSerLySIIeAlaLySIIeLeuPro 100
Db 266 ATCATGGAACCTTCATGACAGATGGGGAACAGGTGCTCAAAATTGCCAAGCATCTACCC 325
Qy 101 GLyATGTrpAspAsnGluIleLeuAsnTyrlTrpArgTrpArgIleGlnLySIIeLeu 120
Db 326 GGAAGGACTGATCTGAGATTAAAGAACTACTGAGAGCAATGATCATGATGACCTCAAG 385
Qy 121 GlnAla 122
Db 386 CAAGCT 391

RESULT 8
US-09-878-574-5021
; Sequence 5021, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
```

```

; SEQ ID NO 5021
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-010-Q1-B1-B1
; US-09-878-574-5021

Alignment Scores:
Pred. No.: 2,056-61 Length: 438
Score: 586.00 Matches: 112
Percent Similarity: 87.05% Conservative: 9
Best Local Similarity: 80.58% Mismatches: 15
Query Match: 51.49% Indels: 3
DB: 10 Gaps: 1

US-10-021-811-36 (1-206) x US-09-878-574-5021 (1-438)
Qy 1 MetAspLySgInGInCysLySThrSerGlnAspProGluValArgLySgLyProTr 20
Db 29 ATGACAAAGAAAGCTTGCG--AACACGCTCATGATCTCGAAGTGAAGAAAGGCGCATGG 88
Qy 20 ThrMetGluGluAspLeuIleLeuMetAsnTyrlleAlaAsnHisgLyGluGlyValTr 40
Db 89 GACAAAGGAAAGAAAGCTTATCTTGATTAACATATGCAAAATCACGGTGAACGTGTTTG 148
Qy 40 PAenSerLeuAlaLySAlaAlaGlyLeuLySArgAsnGlyLySArgCysArgLeuArgTr 60
Db 149 GAACCTCTTAGCCAAAGCTTCTGCTCTCAACGAACGGGAAGAGTTGTCGACTCGTTG 208
Qy 60 PleuAsnTyrlLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
Db 209 GCTAACACTACCTTCGCTCGATGTTAGAAAGAGAAACATTACACCGGGAAGCACTTTT 268
Qy 80 uIleMetGluLeuHisAlaLySArgGlyAsnArgTrpSerLySIIeAlaLySIIeLeuPr 100
Db 269 GATCATTAAGAACTTCATGACAAAGTGGGCAATACGTGCTCAAAATTGCCAAGCATCTTC 328
Qy 100 oGlyATGTrpAspAsnGluIleLeuAsnTyrlTrpArgTrpArgIleGlnLySIIeLeu 120
Db 329 AGGAAGAACTGACAAATGATTTAGAACTTCTGAGAAACAAGATTCAAAACACATTAA 388
Qy 120 gGlnAlaGluAsnPhelGlnGlnInSerSerAsnAsnSerGluIleAsnAspHis 138
Db 389 GCAAGCTGAGACTTCACAAACAT-----GGTAATTCAGAGAAATATGATCAT 437

RESULT 9
US-09-878-574-327
; Sequence 327, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 327
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-052-Q1-B2-D5
; US-09-878-574-327

Alignment Scores:
Pred. No.: 1,216-58 Length: 375
Score: 562.00 Matches: 104
Percent Similarity: 93.28% Conservative: 7
Best Local Similarity: 87.39% Mismatches: 6
```


Query Match: 49.38% Indels: 2
DB: 10 Gaps: 1
US-10-021-811-36 (1-206) x US-09-878-574-327 (1-375)
QY 23 GUGUAAPLeuileLeuMeCAsnTyrlleAlaasnHISglYglUGlYValTTPAsnSer 42
DB 23 GAGAGAGACTTGTCTTATTAATATTCATATTCATCGGTGAAGGTTTGAACCTCC 82
QY 43 LeuAlaYsaAlaAlaGlyLeuLysArgasnGlyLysSerCySaArgLeuAgtTTPLeuasn 62
DB 83 TTAGCCAAAGCTTCGTGCTCAACAGAGGGAAGAGTTTCACCTCCGTGGCTAAC 142
QY 63 TyrlleuArgProaspValArgArgGlyAsnleThrProglUGlUGlLeuileMeC 82
DB 143 TACCTTCCTCGATGTAGAGAGAGAAACATACACCCGAGGAAGCTTTATCATATA 202
QY 83 GUGUeHISAlaYsTTPGlyAsnArgTTPSerYsileAlaYsHISleuProGlyArg 102
DB 203 GAACCTTCATGCAAGATGGGCAATGAGTGTGTCGAAATGCAAGACATCTTCAGGAGAA 262
QY 103 ThrAspangluileLysAsnTyrlTTPArgThArgileglInYsHISleYsGlnAla 122
DB 263 ACTACACATGAGATTAAAGACTTCTGAGAGACAGATCCACAGCATTAAAGCAAGCT 322
QY 123 GluAsnPhgInglInserSerAsnAsnSerGluileAsnAspHISGlnAlaSer 141
DB 323 GAGACTTCACAGAACAT-----GTTATTCAGAGAAATGATCATCAAGCAAGC 373
RESULT 10
US-09-878-574-3147
/ Sequence 3147, Application US/09878574
/ Patent Nc. US20020110548A1
/ GENERAL INFORMATION:
/ APPLICANT: Byrum, Joseph R.
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Thompson, Michael D.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(15401)B
/ CURRENT APPLICATION NUMBER: US/09/878,574
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,535
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 3147
/ LENGTH: 379
/ TYPE: DNA
/ ORGANISM: Glycine max
/ OTHER INFORMATION: Clone ID: LIB3028-015-Q1-B1-E7
US-09-878-574-3147
Alignment Scores:
Pred. No.: 1,86e-58 Length: 379
Score: 560.50 Matches: 104
Percent Similarity: 89.17% Conservative: 3
Best Local Similarity: 86.67% Mismatches: 12
Query Match: 49.25% Indels: 1
DB: 10 Gaps: 1
US-10-021-811-36 (1-206) x US-09-878-574-3147 (1-379)
QY 1 MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTTP 20
DB 23 ATGACACAAAGAGCTTGCC--AACACGTCCTCATGATCTCGAAGTGAAGAGGGGCAATGG 79
QY 21 ThrMetGlnGluAspLeuileLeuMeCAsnTyrlleAlaasnHISglYglUGlYValTTP 40
DB 80 ACATATGAGACATTAATCTTATTCATCACTATATATGCCAATACCGGGAGAGGGGTTTGG 139
QY 41 AsnSerleuAlaYsaAlaAlaGlyLeuLysArgasnGlyLysSerCySaArgLeuArgTTP 60
DB 140 AACTCTTTGGCCAAAGCTGTGAGATTAAACGTAACCGAGAAAGAGTTGCCGGCTCCGGTGG 199

QY 61 LeuAsnTyrlleuArgProaspValArgArgGlyAsnleThrProglUGlUGlLeuLeu 80
DB 200 CTAAACTACCTCCGCTCTGATGTAGAGAGGAGATATTACCCGAGAGAACGCTTTGG 259
QY 81 IleMetGluLeuHISAlaYsTTPGlyAsnArgTTPSerYsileAlaYsHISleuPro 100
DB 260 ATCATGAGACTTCATGCAAGATGGGGAACAGGTGTCCAAATATGCGAAGATCTACCC 319
QY 101 GlyArgThrAspAsnGluileLysAsnTyrlTTPArgThArgileglInYsHISleYs 120
DB 320 GGAAGAGACTGATTAATGAGATTAGACTTACGACGACAGATCCATTAAGCACTCAAG 379
RESULT 11
US-09-878-574-50
/ Sequence 50, Application US/09878574
/ Patent No. US20020110548A1
/ GENERAL INFORMATION:
/ APPLICANT: Byrum, Joseph R.
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Thompson, Michael D.
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(15401)B
/ CURRENT APPLICATION NUMBER: US/09/878,574
/ CURRENT FILING DATE: 2001-12-21
/ PRIOR APPLICATION NUMBER: 09/333,535
/ PRIOR FILING DATE: 1999-06-14
/ NUMBER OF SEQ ID NOS: 15775
/ SEQ ID NO 50
/ LENGTH: 350
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1) ..(350)
/ OTHER INFORMATION: unsure at all n locations
/ OTHER INFORMATION: Clone ID: LIB3028-056-Q1-B1-G4
US-09-878-574-50
Alignment Scores:
Pred. No.: 4.98e-58 Length: 350
Score: 556.50 Matches: 103
Percent Similarity: 93.69% Conservative: 1
Best Local Similarity: 92.79% Mismatches: 6
Query Match: 48.90% Indels: 1
DB: 10 Gaps: 1
US-10-021-811-36 (1-206) x US-09-878-574-50 (1-350)
QY 1 MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTTP 20
DB 16 ATGACACAAAGAGCTTGCC--AACACGTCCTCATGATCTCGAAGTGAAGAGGGGCAATGG 72
QY 21 ThrMetGlnGluAspLeuileLeuMeCAsnTyrlleAlaasnHISglYglUGlYValTTP 40
DB 73 ACATATGAGACATTAATCTTATTCATCACTATATATGCCAATACCGGGAGAGGGGTTTGG 132
QY 41 AsnSerleuAlaYsaAlaAlaGlyLeuLysArgasnGlyLysSerCySaArgLeuArgTTP 60
DB 133 AACTCTTTGGCCAAAGCTGTGAGATTAAACGTAACCGAGAAAGAGTTGCCGGCTCCGGTGG 192
QY 61 LeuAsnTyrlleuArgProaspValArgArgGlyAsnleThrProglUGlUGlLeuLeu 80
DB 193 CTAAACTACCTCCGCTCTGATGTAGAGAGGAGATATTACCCGAGAGAACGCTTTGG 252
QY 81 IleMetGluLeuHISAlaYsTTPGlyAsnArgTTPSerYsileAlaYsHISleuPro 100
DB 253 ATCATGAGACTTCATGCAAGATGGGGAACAGGTGTGCCAAATATGCGAAGATCTACCC 312
QY 101 GlyArgThrAspAsnGluileLysAsnTyrlTTPArgThArgileglInYsHISleYs 111
DB 313 GGAAGAGCTGATTAATGAGATTAAAGACTACTGG 345

RESULT 12
US-09-878-574-194
Sequence 194, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401)B
CURRENT APPLICATION NUMBER: US/09/878, 574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333, 535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 194
LENGTH: 365
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-054-Q1-B1-B1
US-09-878-574-194

Alignment Scores:
Pred. No.: 1,1e-56 Length: 365
Score: 545.50 Matches: 102
Percent Similarity: 93.64% Conservative: 1
Best Local Similarity: 92.73% Mismatches: 6
Query Match: 47.93% Indels: 1
DB: 10 Gaps: 1

US-10-021-811-36 (1-206) x US-09-878-574-194 (1-365)

QY 1 MetAspIySlySGInGInCylserThrSerGlnAspProGluValArgLysGlyProTTrp 20
DB 37 ATGGACAAAGAACTTGGC--AACACGCTCATGATCTCTGAAGTGAAGAGGGGCGCATGG 93
QY 21 ThrMetGluGluAspLeuIleuMetAsnTyrIleAlaAsnHisGlyGluGlyValTTrp 40
DB 94 ACNATGGAAGAGACTTAAATCTTGAATCCTTATTCACCTTATTCGCAATTCACGGGGAAGGGTTTGG 153
QY 41 AsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTTrp 60
DB 154 AACTCTTTGGCCCAAGCGCTGCTGACTTAAACGTACCGGAAAGATTGCCGCTCGGCTGG 213
QY 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGluLeu 80
DB 214 CTAAACTACCTCCGCTCGTGAATGTTGAAGAGGGAATATTACCCCGAAGAACAGCTTTTG 273
QY 81 IleMetGluLeuHisAlaLysTTrpGlyAsnArgTTrpSerLysIleAlaLysHisLeuPro 100
DB 274 ATCATGGAACCTTCATGCAAGATGGGGAACAGGTGCTCCAAATATTCGCAAGCATCTACCC 333
QY 101 GlyArgThrAspAsnGluIleLysAsnTyr 110
DB 334 GGAAGGACTGATATGAGATTAAAGACTTAC 363

RESULT 13
US-10-021-811-45
Sequence 45, Application US/10021811
Patent No. US20030024007A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fang, Yiwen
APPLICANT: Odell, Joan
APPLICANT: Weng, Zude
TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
FILE REFERENCE: BA1294 US NA
CURRENT APPLICATION NUMBER: US/10/021, 811
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: 60/110,609
PRIOR FILING DATE: 1998-December-02

NUMBER OF SEQ ID NOS: 63
SOFTWARE: Microsoft Office 97
SEQ ID NO 45
LENGTH: 1236
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (519)
NAME/KEY: unsure
LOCATION: (521)
NAME/KEY: unsure
LOCATION: (530) . (531)
NAME/KEY: unsure
LOCATION: (534)
NAME/KEY: unsure
LOCATION: (800)
NAME/KEY: unsure
LOCATION: (1124)
NAME/KEY: unsure
LOCATION: (1151)
US-10-021-811-45

Alignment Scores:
Pred. No.: 8.25e-54 Length: 1236
Score: 528.00 Matches: 103
Percent Similarity: 68.06% Conservative: 27
Best Local Similarity: 53.93% Mismatches: 43
Query Match: 46.40% Indels: 18
DB: 9 Gaps: 4

US-10-021-811-36 (1-206) x US-10-021-811-45 (1-1236)

QY 1 MetAspIySlyS-----GInGInCylserThrSerGlnAsp 12
DB 96 ATGATGAAAGAAAGAGACAGAAATGACACACCTTTAAAGTTGTAGAGACAGATGAC 155
QY 13 ProGluValArgLysGlyProTTrpThrMetGluGluAspLeuIleuMetAsnTyrIle 32
DB 156 -----CTTGAAGAGAGCCCTTGACCGTGCATGAAAGACCTCATCTTATTAATTAATT 209
QY 33 AlaAsnHisGlyGluGluValArgTTrpAsnSerLeuAlaLysGlyLeuLysArgAsn 52
DB 210 GCCACTCATGCGCAAGAGTGTGCTGGAACAGCTGCGCTCTGCTGGGTGGAAGCAAGC 269
QY 53 GlyLysSerCysArgLeuArgTTrpLeuAsnTyrLeuArgProAspValArgArgGlyAsn 72
DB 270 GGGAGAGATTGCAATTTGAGAGTGGCTGAATTAATCTGCTGCTGATTTGACCTGGAAGC 329
QY 73 IleThrProGluGluGluLeuLeuIleMetGluLeuHisAlaLysTTrpGlyAsnArgTTrp 92
DB 330 ATCAGCACTTGAAGACAACTTTGATTCTGAGACTTCATTTCTGCTGGGGAACCGTTGG 389
QY 93 SerLysIleAlaLysHisLeuProGlyArgTTrpAspAsnGluIleLysAsnTyrTTrpArg 112
DB 390 TCGAAATATTCCTAATAATTTGCTGTTGAGAACCGAACAAGATTAAGAACTAATTTGAGA 449
QY 113 ThrArgIleGlnLysHisIleLysGlnAlaGlu-----AsnProGlnGlnGlnIns 129
DB 450 ACCGGTCTCAAAAGCATGCGCAAGCAACTCAAAATGCACTGATTAAGCAAGCAATTCAG 509
QY 130 SerAsnAsnSerGluIleAsnAspHisGlnAlaSerThrSerHisValSerThrMetAla 149
DB 510 GACACCATGNGNTACTTTGNNATNCCAAAGGCTGCGAAGCATTCACAGACGGCGAC 569
QY 150 GluProMetGluMetLys-----SerProGlySerTyrGlnGlyMetLeu 164
DB 570 GGGCCCGCTAACCAACCGCTAACTGGCGGCGCCACCAACATGATTCACCTAAGGAAA 629
QY 165 GluProPheSerThrGlnPheProThrIleAsn 175
DB 630 CAACCTTATACCAACCAATTCAGAGTTTGAAT 662

```
RESULT 14
US-10-021-811-17
; Sequence 17, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odeh, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: B01294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 17
; LENGTH: 587
; TYPE: RNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (577)
; NAME/KEY: unsure
; LOCATION: (582)..(583)
; NAME/KEY: unsure
; LOCATION: (587)
US-10-021-811-17

Alignment Scores:
Pred. No.: 2.86e-53      Length: 587
Score: 519.50           Matches: 94
Percent Similarity: 77.24% Conservative: 18
Best Local Similarity: 64.83% Mismatches: 14
Query Match: 45.65%      Indels: 19
                        Gaps: 2
DB: 9

US-10-021-811-36 (1-206) x US-10-021-811-17, (1-587)

QY 14 GluValArgLysGlyProTTPThMetGluGluAspLeuLeuMetAsnTyrIleAla 33
Db 77 GAGCTCCGCGCAGAGGCGCTGACGCTGAGAGGAGACCTGCTCTTCGCACTACATGCC 136
QY 34 AsnHisGlyGluGlyValTTPAsnSerLeuAlaLysAlaIleGlyLeuLysArgAsnGly 53
Db 137 GCCCATGCGCAGGCGCGCTGGAGACGCGCTGCGCGCGCTGGAAGCGGAGCGGG 196
QY 54 LysSerCysArgLeuAspArgTTPLeuAsnTyrLeuAspProAspValArgArgGlyAsnIle 73
Db 197 AAGAGCTGCGCGCTGCGCTGCTGACTAAGCGCGGAGCTGAGAGAGGAGGAGAACATG 256
QY 74 ThrProGluGluGluLeuLeuIleMetGluLeuHisAlaLysTTPGlyAsnArgTTPSer 93
Db 257 ACGGCGGAGGAGGAGCGCTGATGATGAGAGCTCCATGCGGCGGGGAGATCGGTGAGC 316
QY 94 LysIleAlaLysHisLeuProGlyArgThrAspAsnGluIleLysAsnTyrTTPArgTThr 113
Db 317 AAGATCCGCGAGCATCTCCCGCGCGGACGACGACAGCAAGATCAAGAACTACGCGGACC 376
QY 114 ArgIleGluLysHisIleLysGlnAlaGluAspNheGlnGlnInSerSerAsnAsnSer 133
Db 377 CCGCTCCAGAGCAGCGCAGCAAGCACTC-----AACTGC 409
QY 134 GluIleAsnAspHisGln-----AlaSerThrSer 143
Db 410 GAGCTCAACTCCAGCGATTCACAGACCTATGCGCTACTCTTGATGCCCGCTCTCTCG 469
QY 144 HisValSerThrMet 148
Db 470 AACGCATCAACGCTC 484
RESULT 15
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US-10-021-811-47
; Sequence 47, Application US/10021811
; Publication No. US20030024007A1
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Fang, Yiwen
; APPLICANT: Odeh, Joan
; APPLICANT: Meng, Zude
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
; FILE REFERENCE: B01294 US NA
; CURRENT APPLICATION NUMBER: US/10/021,811
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/110,609
; PRIOR FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Microsoft Office 97
; SEQ ID NO: 47
; LENGTH: 1181
; TYPE: DNA
; ORGANISM: Glycine max
US-10-021-811-47

Alignment Scores:
Pred. No.: 1.06e-52      Length: 1181
Score: 518.50           Matches: 117
Percent Similarity: 48.21% Conservative: 31
Best Local Similarity: 38.11% Mismatches: 52
Query Match: 45.56%      Indels: 107
                        Gaps: 9
DB: 9

US-10-021-811-36 (1-206) x US-10-021-811-47 (1-1181)

QY 3 LysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTTPThMet 22
Db 34 AAGAGCTGACGAGCTTCTGAGTGAAGATGACATGAACTTAAGAGGCGCTTGACCTCG 93
QY 23 GluGluAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluGlyValTTPAsnSer 42
Db 94 GAAAGAGATTAAGCTTCTCCCATATATTTTATATCATGGGAGGCGCATGGAATTGG 153
QY 43 LeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuArgTTPLeuAsn 62
Db 154 CTGGCTTAAACGTTTCAGATTAAAGAGAACTGGGAAAGTTGCACAAATTAAGCTGCTAAAT 213
QY 63 TyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeuLeuIleMet 82
Db 214 TATCTAAAGCCAGAGTGAATAAGCGGGAATTTAACCCACAGAGCAATTTATATTCTT 273
QY 83 GluLeuHisAlaLysTTPGlyAsnArgTTPSerLysIleAlaLysSleuProGlyArg 102
Db 274 GAACTCCACTCAAAAGTGGGAAACAGGTGCTCAAAAAATTGCACAAATTTGCCAGCGAGA 333
QY 103 ThrAspAsnGluIleLysAsnTyrTTPArgThrArgIleGlnLys-----HisIle 119
Db 334 ACAAGCATGAAATCAAGAACTATTGGAGAACTGCAATTCAGAAACAAGCAAGCATTTG 393
QY 120 Lys-----GlnAlaGluAspNheGln----- 126
Db 394 AAAATTTACTGACAGCAGAGAGCTTCAAGAACTTTGAGCGCTTTCTGAGATGCCCTAGA 453
QY 127 -----GlnGlnSerSerAsnAsnSerGluIleAsnAspHisGlnAla 140
Db 454 TTGCTTCAGAAAGCAAAAGATCATCTTTTCACAAAGTGCATTT-----CAAAACAGGCA 510
QY 141 SerThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCysTyr 160
Db 511 ATTCTTAGCTTTTGAATTATGATTTCTCAGCATTTTACTGTGGACCATATCTCTCTGG 570
QY 161 GlnGly-----MetLeuGluProPheSerThr-----GlnPhePro 172
Db 571 CAGGAGCTTGTATGAATGAAGCTGTCCCATTTACATGAGCAACATGAGAGACTCAG 630
QY 173 ThrIleAsnProAspGlnSerSerCys----- 182
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Db 631 ACTCGAACACCAACATGGTTTCATGCATCTCTTGTCGAGTCAGCAAAATATTCAAAA 690
Qy 183 -----
Db 691 GTGCCTCAGCATTTTGGACACACCAATTCATGCTGAAATACCAATGAC 750
Qy 186 -----
Db 751 TTTGGACCTTCACATATGAAAGTTATATGTAACACACATGCTATGAGATGACAAAC 810
Qy 189 -----
Db 811 TTCAAAAGACTACTACATGGGTGGCTGAGATGGCAATACCAATTGTGATTGTCAA 870
Qy 190 -----
Db 871 ATGTAGAGAGCAATTGGGTAAACACAGATTTTGATGTATGATGTGACATGATGAA 930
Qy 197 SerTyrSerMetGlnLeuIeu 203
Db 931 CTGTGGCAGTTTAGCAGTTA 951
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Search completed: February 8, 2003, 12:31:45
Job time : 62 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 8, 2003, 11:07:20 ; Search time 1928 Seconds

(without alignments)
1730.431 Million cell updates/sec

Title: US-10-021-811-36

Perfect score: 1138

Sequence: 1 MDRKQCKTSQDPEVRKGPW.....NNINYSMEDSNMQLLNGD 206

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 809774376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPTO.spool/US10021811/runat.03022003.111222.25647/app.query.fasta.1.391
-DB=EST -QPM=fastcap -SURFXX=1st -MIMATCH=0.1 -FOOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US10021811 @cgn.1.1.1349 @runat.03022003.111222.25647 -NCPU=6 -ICPU=3
-NO XLPXY -NO MAMP -LARGEOBFRY -NEG SCORES=0 -WAIT -LONGLOG -DEV TIMEOUT=120
-WARM TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: gb_gsa:*
18: em_gsa_hum:*
19: em_gsa_inv:*
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23: em_gsa_mam:*
24: em_gsa_mus:*
25: em_gsa_other:*
26: em_gsa_pro:*
27: em_gsa_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991	87.1	562	14	BM732121 sal173b11.1
2	859.5	75.5	635	14	BM146360 NPO47E06F
3	851	74.8	501	13	BM527606 sal63g06.
4	846	74.3	782	10	BE68316 CM700005B
5	816	71.7	552	13	BM527774 sal65g03.
6	813.5	71.5	560	14	BM732539 sal178e08.
7	808	71.0	682	12	BM457971 NFO37A10P
8	796	69.9	669	14	BM146831 NFO28G06F
9	795.5	69.9	568	13	BM527664 sal64d10.
10	784	68.9	523	9	A1930997 BM45h07.Y
11	784	68.9	688	13	B1272897 NFO91A12F
12	779.5	68.5	544	13	BM527508 sal62f08.
13	774.5	68.1	542	13	BM528383 sal157E09.
14	724	63.6	681	9	A1486576 BM5244897
15	709.5	62.3	476	10	BE057370 SM02C04.Y
16	673.5	59.2	592	10	AM928236 EST307029
17	671	59.0	558	10	BE324639 NFO24C04P
18	670.5	58.9	470	10	AM156542 se28d11.Y
19	657	57.7	409	12	BE804790 se45f11.Y
20	654.5	57.5	425	10	AM423958 BH58605.Y
21	642	56.4	503	14	BQ104458 981307.e
22	639	56.2	500	9	A1897784 EST267227
23	639	56.2	519	9	A1897681 EST267124
24	637.5	55.0	502	14	BQ106505 IC0568.e
25	627.5	55.1	447	13	B1273011 NFO97F02F
26	621	54.6	395	12	BE805071 se37a07.Y
27	614	54.0	450	10	BE058947 SM23b01.Y
28	601	52.8	431	10	AM459279 B122h08.Y
29	595	52.3	586	12	BE820766 CM7000012A
30	593	52.1	715	10	BE658737 CM700007A
31	529.5	46.5	542	9	AU238946 AU238946
32	527	46.3	397	10	AM432364 BH73a04.Y
33	526.5	46.3	727	12	BG607379 WHE2471.H
34	522.5	45.9	676	14	BU013207 BF649523
35	514	45.2	765	10	BE659054 CM700008A
36	514	45.2	635	10	AM032656 EST276215
37	513.5	45.1	690	14	BQ147546 NFO41H09F
38	513.5	45.1	605	13	BU233398 B1233398
39	511	44.9	370	12	BG642441 EST355917
40	510	44.8	371	9	A1487923 EST246245
41	508	44.6	502	10	BE459188 EST414480
42	508	44.6	566	13	B1424418 sal634e05.
43	506.5	44.5	510	12	BF325282 SM20e03.Y
44	506	44.5	536	13	B1701275 sal65g08.
45	501	44.0			

ALIGNMENTS

RESULT 1
BM732121
LOCUS
DEFINITION
Gm-c1061-4678 5' similar to TR:Q39028 Q39028 ATMYB2. ; mRNA
sequence.
ACCESSION
BM732121 GI:19053454
VERSION
BM732121.1
KEYWORDS
SOURCE
ORGANISM
Glycine max
soybean.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

ORGANISM
glycine max
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;
Glycine.

REFERENCE
1 (bases 1 to 552)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna,
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE
JOURNAL
COMMENT
Public Soybean R/Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: RegGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@reggen.com web site:
www.reggen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 426.
Location/Qualifiers

FEATURES
source
1..552
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4134"
/clone_1lb="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants for the cultivar
Raiden. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."

BASE COUNT
184 a 118 c 111 g 139 t

ORIGIN

Alignment Scores:
Pred. No.: 1.05e-85 Length: 552
Score: 816.00 Matches: 152
Percent Similarity: 95.62% Conservative: 1
Best Local Similarity: 95.00% Mismatches: 5
Query Match: 71.70% Indels: 2
Gaps: 2

US-10-021-811-36 (1-206) x BM527774 (1-552)

Oy 49 leulyaarganglylvysserCyargyleuargtTPlleuanryTleuargProaspva1 68
Db 1 CTCAACGTAACCGAAGAGTTCGCGCTAAGGTGCTAACTACCTCGTCGTATTT 60
Oy 69 AAGAGGAGAAATTTCTThProglunglnleuenu1emerGluLeuHialalyerTrp 88
Db 61 AAGAGGAGAAATTTCTThProglunglnleuenu1emerGluLeuHialalyerTrp 120
Oy 89 GAAAGATGTPSerlysllealalyshlsleuProglYargThAspAsnglu1lelyS 108
Db 121 GGAACAGGTGTCGCAAAATTCGCAAGCATCTACGTGAGACAGATTAAGATCAAG 180
Oy 109 AenryTTPargThArgllleGlnlyshlslelyGlnAlaGluasnPhelnglnln 128

Db 181 AACTATTGAGAGCAGATCCAGAGCATCAAGAGTGAAGACTTTCAGACAA 240
Oy 129 SerSerAsnAsnSerGlu1leAsnaphisglnAlaserThrsleValserThrmet 148
Db 241 ATTAGTATATCTTGAGATATATATATATATATATATATATATATATATAT 300
Oy 149 AlagluProMetGluMetlyserProProCyaryTglnlyMetleuGluProPheSer 168
Db 301 GCTGAACCATGAGACCATATATCTCACCTTTATCAAGAAATGTATAGACCATTTTCT 360
Oy 169 Thr---GlnPheProThrlleAsnProaspGlnSerSerCyseThAsnAspAsn 187
Db 361 TCATATCAATTCCTCCACCAATTAATCTTATCAATCAATGTTGACCAACAAAC 420
Oy 188 Aasn---lAenryTTPSerMetGluAspSerTPSerMetGlnleuAsnGlyasp 206
Db 421 AACAGATTATATTTGAGCATGAGCATATCTGTCAATCAATCTGATCAACGGGAT 480

RESULT 6
BM732539
LOCUS
560 bp mRNA linear EST 01-MAR-2002
DEFINITION
gsl78e08.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN CLONE ID:
Gm-c1061-5223 5' similar to TR:Q39028 Q39028 ATMB2. ;, mRNA
sequence.

ACCESSION
BM732539
VERSION
BM732539.1 GI:19053872
KEYWORDS
EST.

SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE
1 (bases 1 to 560)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Coryell, V., Khanna,
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers,
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk,
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,
R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: RegGen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@reggen.com web site:
www.reggen.com
Seq primer: -40RP from Gibco
High quality sequence stop: 430.
Location/Qualifiers

FEATURES
source
1..560
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-5223"
/clone_1lb="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants for the cultivar
Raiden. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The


```

Db      527 ACAATATTATATACACCTCTTACCAAGAAATTTTGAACCAATTCACCTCATCAT 586
Qy      170 GlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsn189
Db      587 CAGTTCCTCCATCAATCTCT---GATCAATCAAGTTGTCTCT-----622
Qy      190 AsnTyTrpSerMetGluAspSerTrpSerMetGlnLeuLeuAsn 204
Db      623 AACTACTGAGACATGGAAGATCTCTGTCTCACTCACTCACTAAAT 667

RESULT 8
LOCUS   B0146831 682 bp mRNA linear EST 24-APR-2002
DEFINITION NF028G06FL1J051 Developing flower Medicago truncatula cDNA clone
ACCESSION B0146831
VERSION   B0146831.1 GI:20283890
KEYWORDS EST.
SOURCE   barrel medic.
ORGANISM Medicago truncatula
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
           Medicago.
REFERENCE 1 (bases 1 to 682)
AUTHORS   Torres-Gerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
           Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
           Expressed Sequence Tags from the Samuel Roberts Noble Foundation
           Medicago truncatula flower library
           Unpublished (2001)
JOURNAL   Contact: May GD
           Plant Biology Division
           The Samuel Roberts Noble Foundation
           2510 Sam Noble Parkway, Ardmore, OK 73402, USA
           Tel: 580 221 7391
           Fax: 580 221 7380
           Email: gdmay@noble.org
           Insert length: 682 Std Error: 0.00
           Plate: 028 row: G column: 06
           Seq primer: TCACACGAGAAACAGCTATGAC.
           Location/Qualifiers
FEATURES
     source
         1..682
            /organism="Medicago truncatula"
            /db_xref="taxon:3880"
            /clone="NF028G06FL"
            /clone_lib="Developing flower"
            /tissue_type="Developing flowers"
            /dev_stage="Developmentally pooled. Contains a mixture of
            very young, developing, fully-opened flowers and flowers
            in early transition into pods."
            /note="Vector: Lambda Zap; cDNA was prepared from polyA-
            enriched, pooled samples of equivalent amounts of total
            RNA from very young, developing, fully-opened flowers and
            flowers transitioning into pods. The cDNA was
            directionally ligated into the Uni-Zap XR vector
            (Stratagene) and packaged using the GigaPack III Gold
            packaging extracts. Phagemids containing cDNA inserts were
            in vivo excised from the recombinant Uni-Zap XR vector
            using ExSist helper phage and the E. coli strain
            XL1-Blue MRF' (Stratagene). Excised plasmids were plated
            using SOLR cells."
BASE COUNT 230 a 142 c 128 g 180 t 2 others
ORIGIN
Alignment Scores: 3.29e-83 length: 682
Score: 796.00 matches: 160
Percent Similarity: 81.19% conservative: 17
Best Local Similarity: 73.39% mismatches: 20
Query Match: 69.95% indels: 21
DB: 14 gaps: 7

```

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US-10-021-811-36 (1-206) x B0146831 (1-682)
Qy      1 MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTrp 20
Db      47 ATGGACAAATAAA---GAGTGCAGTTCTTACAAAGATCTGTATGACGAAGGACCATGG 103
Qy      21 ThrMetGluGluAspLeuLlleuMetCAsnTyTrlIleAlaAsnHlaGlyGluGlyValTrp 40
Db      104 ACAATGGAAGAGACCTTATCTTGATCTTGATCACTATATGTGCATATCGGAAGGGTGTGG 163
Qy      41 AsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCysArgLeuAspTrp 60
Db      164 AACTCTTGCTGCTAAATCTGCTGCTTGAACCTACCGAAGAGAGTTGACGCTTCGGTGG 223
Qy      61 LeuAsnTyTrLeuArgProAspValArgArgLysAsnIleThrProGluGluGlnLeuLeu 80
Db      224 CTTAACTATCTTCGACCGGATGTTAGACGAGGAATATTACACCTGAGGAACAATCTTGG 283
Qy      81 lMetGluLeuHlaLysAlaLysTrpGlyAsnArgTrpSerLysIleAlaLysHlaLeuPro 100
Db      284 ATCATTTGAACCTTCATGCTTAAGTGGGAAACAGTGTGGAATTCGCAACATCTTACCG 343
Qy      101 GJArgTrpAspAsnGluLlleLysAsnTyTrpArgTrpArgLleGlnLysHlaLys 120
Db      344 GGAAGAACCGATTAATGATGAATAAGAACTACTGAGAGACAGAGATCCAAAGCATATTCAG 403
Qy      121 GlnAlaGluAsnPhenGln---GlnGlnSerSerAsnAsnSerGluIleAsnAspHlaGln 139
Db      404 CAAGCTGGAATCTTCATATCTCAACAGAGTCTGATATTCAATTAATGAATGATATAT 463
Qy      140 -----AlaSerThrSerHlaValSerThrMetAlaGluProMetGln 153
Db      464 AATTAATTAATCACTTAATGAGGAACAGCAAGCAATTTCCAAATGCTGGAACCTATGGA 523
Qy      153 u-----MetTySerProProCysTyGlnGlyMetLeuGluProPheSerThr----- 169
Db      524 CACAAATATTATATATACACCTCTTACCAAGAAATTTTGAACCATTTCCACCTCATCA 583
Qy      170 -GlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsn11 189
Db      584 TCAAGTTCCTCCATCAATCTCT---GATCAATCA-----GGTTGATC 619
Qy      189 eAsnTyTrpSerMetGluAspSerTrpSerMetGlnLeuLeuAsnGlyAsp 206
Db      620 TAACTACTGAGACATGGAAGATCTCTGTGCACTTCACTCACTAAATGAGAT 671

RESULT 9
LOCUS   BM527664 568 bp mRNA linear EST 19-FEB-2002
DEFINITION sal64d10.y1 Gm-c1061 Glycine max cDNA clone SOYBEAN C1061 ID:
           Gm-c1061-4003 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mRNA
           sequence.
ACCESSION BM527664
VERSION   BM527664.1 GI:18733532
KEYWORDS EST.
SOURCE   soybean.
ORGANISM Glycine max
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Rosidae; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
           Glycine.
REFERENCE 1 (bases 1 to 568)
AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
           ,A., Bolla,B., Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
           Wylie,T., Underwood,K., Stepcoe,M., Theising,B., Allen,M., Bowers
           ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
           ,R., Ritzer,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
           ,R., Waterston,R. and Wilson,R.
           Public Soybean EST Project
           Unpublished (1999)
JOURNAL   Contact: Shoemaker R/Public Soybean EST Project
           Public Soybean EST Project
           Washington University School of Medicine

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site: www.resgen.com

Seq primer: -40RP from Gdbco
High quality sequence stop: 422.

FEATURES

SOURCE

1-568
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1061-4003"
/clone_id="Gm-c1061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The cDNA library was constructed from mRNA isolated from mature flowers of field grown plants for the cultivar Ralden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT

174 a 134 c 124 g 136 t

Alignment Scores:

Pred. No.: 2.85e-83 Length: 568
Score: 795.50 Matches: 153
Percent Similarity: 87.91% Conservative: 7
Best Local Similarity: 84.07% Mismatches: 19
Query Match: 69.90% Indels: 3
DB: 13 Gaps: 3

US-10-021-811-36 (1-206) x BM527664 (1-568)

QY 1 MetAspLysLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTyr 20
Db 29 ATGGACAAAGAGCTTGCG--AACACGCTCATGATCTCTGAAGTGAAGAAAGGGCCATGG 85
QY 21 ThrMetGluLysAspLeuIleLeuMetAsnTyrIleAlaAsnHisGlyGluValTyr 40
Db 86 ACAAAGGAAGAAAGCTTAATCTTGAATCACTATATTTGCCATATCAGGGGAAGGGGTTGG 145
QY 41 AsnSerLeuAlaLysAlaLysGlyLeuLysArgAsnGlySerCysArgLeuArgTyr 60
Db 146 AACCTTTGGCGAAGGCGCTGAGCTTAACGTACCGGAAGAGTTGCCGCTCCGGTGG 205
QY 61 LeuAsnTyrLeuArgProAspValArgArgLysAsnIleThrProGluGluGlnLeu 80
Db 206 CTAAACCTACCTCCGCTCGATGTTAGAGAGGAAATTTAACCCCGAGAAACACCTTTTG 265
QY 81 IleMetGluLeuHisAlaLysTyrGlyAsnArgTyrSerLysIleAlaLysHisLeuPro 100
Db 266 ATCATGAACTTCATGCAAGAGTGGGAAACAGGTGCTCAAAATTTGCCAAGCATCTACC 325
QY 101 GlyArgThrAspAsnGluIleLysAsnTyrTTPArgThrArgIleGlnLysHisLys 120
Db 326 GAAAGGACTGAATTAAGAACTAATGAGGAGCAAGAGATCCCAAGACACTTCAG 385
QY 121 GlnAla--GluAspHepGlnGlnSerSerAsnAsnSerGluIleAsnAspHisGln 139
Db 386 CAAAGCTTCACAGACTTCACCAACAGAGTAGTATCTGAGATTAATTATCATCCCAA 445
QY 140 AlasThrSerHisValSerThrMetAlaGluProMetGluMetTyrSerProProCys 159

Db 446 GCTTGACATGACCAAGTATGCCATGCGGACGCCCATAGAAACCTATTTCACCCAGT 505

QY 160 TyrGlnGlyMetLeuGluProPheSerThrGlnPheProThrIleAsnProAspGlnSer 179

Db 506 TATCAAGAGATGTTAGATCATTTTCATATTCAGTTCCCAACA--AATTCATCATCTTCT 562

QY 180 SerCys 181

Db 563 AGTTGT 568

RESULT 10

LOCUS

Al930997 523 bp mRNA linear EST 30-NOV-2001
gb45h07.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-278 5' similar to TR:Q39028 Q39028 ATMYB2.1, mRNA
sequence.

ACCESSION Al930997 GI:566961

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gdbco
High quality sequence stop: 422.

FEATURES

source

1-523
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1015-278"
/clone_id="Gm-c1015"
/tissue_type="mature flowers, field grown plants"
/lab_host="XL10-Gold"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a blunt restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."

BASE COUNT

172 a 124 c 111 g 115 t 1 others

ORIGIN

Alignment Scores: 5.68e-82 Length: 523
Pred. No.: 5.68e-82

Score:	784.00	Matches:	146
Percent Similarity:	94.84%	Conservative:	1
Best Local Similarity:	94.19%	Mismatches:	8
Query Match:	68.89%	Indels:	0
DB:	9	Gaps:	0

US-10-021-811-36 (1-206) x AI930997 (1-523)

Qy	1	MeAspIySLySLyGInGInCySLySLyThSerGInaSPProGInVAlAGLySLyPProT	20
Db	58	ATGATATAAAAAACAACGTGTACACACGCTCTCAATATCTTAAGTGAAGAAAGACCTTGG	117
Qy	21	ThrMetGInGInaSPleuIleLeuMetAsnTyrlleAlaSnHISGlyGInGlyValTyr	40
Db	118	ACGATGGATATAGACTTGGATTTTATATCACTATATTGGCAATCTATGGGGAAGGCTTTGG	177
Qy	41	AsnSerLeuAlaLysAlaAlaGlyLeuLysArgAsnGlyLysSerCyArgLeuArgTyr	60
Db	178	AATCTTTGGCCAAAGCTGCTGGTCTCAAAAGTACCGAAAGATTTCCCGCTAAGGTGG	233

[illegible]

RESULT 11	LOCUS	DEFINITION
BI272897	BI272897	608 bp mRNA linear EST 18-JUL-2001
	NF091A12FL1088	Developing flower Medicago truncatula cDNA clone
	NF091A12FL 5'	5' , mRNA sequence.

VERSION	BI272897.1	GI:14883621
KEYWORDS	EST.	
SOURCE	barrel medic.	
ORGANISM	Medicago truncatula	

Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae, Medicago.

REFERENCE
1 (bases 1 to 688)
Torres-U'rez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., et al. 1997. The human genome: a reference sequence. *Science* 275: 208-213.

TITLE
Medicago truncatula flower library
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Floties, H.K., Inman, J.T., Waller, J.W. and May, G.D.
1993-1994 (2000)

Journal
unpublished (2001)
Contact: May GD
Plant Biology Division

Franc Biology Division,
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
tel. 680 221 7391

TEL: 580 221 7332
FAX: 580 221 7380
Email: odmav@noble.org

Insert Length:	688	Std Error:	0.00
Plate:	091	row:	A
		column:	12
Seq primer:	TCACACAGGAAACAGCTATGAC.		

FEATURES	Location/Qualifiers
source	1. .688

/organism="Medicago truncatula"

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/db xref="taxon:3880"
/clone="NF091A12FL"
/clone_lib="Developing flower"
/tissue_type="Developing flowers"
/dev stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
/notes="Vector: Lambda Zap, cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-Zap XR vector using ExSist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

```

Alignment Scores:	
Pred. No.:	8,61e-82
Score:	784.00
Percent Similarity:	81.57%
Best Local Similarity:	72.81%
Query Match:	68.89%
DB:	13
	Gaps: 7

1 MetAspLysGlnGlnCysLysThrSerGlnAspProGluValArgLysGlyProTrp 20
QY

49 ATCGACAAAAA---GAGTGCAGTTCTTCACAAAGATCCTGATGTACGAAAGGACCATGG 105

[illegible]

41 AsnSerLeuAlaIysAlaIaIagIleuLysArgAsnGlyLysSerCysArgLeuArgTrp 60

Db 166 AACCTTGCTAAATCTGCTGCTTAAACGTAACCGAAGAGTTGCAGGCTTCGGTGG 225

Qy 61 LeuAsnTyrLeuArgProAspValArgArgGlyAsnIleThrProGluGluGlnLeu 80
nb 226 CTTAACTCTCTTGAACCGATGTTTGAAGAGGGAATATTACACTGGAGAACACTTTG 285

```

20  81 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
21  82 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
22  83 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
23  84 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
24  85 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
25  86 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
26  87 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
27  88 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
28  89 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
29  90 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
30  91 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
31  92 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
32  93 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
33  94 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
34  95 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
35  96 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
36  97 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
37  98 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
38  99 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;
39  100 [element] if not (a1[a1.vstr] < val) then a1.vstr := vstr;

```

286 ATCAATTGAACCTCATGCTTAAGTGGGGAAA CAGGTGTCGAAAATTGCGAAACATCTACCG 345

QY 101 GlyArgThrAspAsnGluIleLysAsnTyrTrpArgThrArgIleGlnLysHisIleLys 120

Db	346	GGAGAACCGATATGAGATTAAACAATTCTGGAGGACACAGGATCCAAAAGCATATCAG	405
Qy	121	GlnAlaGluAsnMheGln---GlnGlnSerSerAsnAsnSerGluIleAsnAspHisGln	139

Db 406 CAAGCTGAGACTTCTAATCTCAGAACAAGTTTGATATTCAATAAATGATGTAAT 465

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QY      140 -----AlaserThSerHisValSerThMetAlagUprometGlu 153
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Db 466 AATAATATCACTATAGGAGCACAAGCCAAATTCACACATTGCGAACCAAGAC 525

Oy	-----MethylserProProCysIyringilwctLengidupPheSerImr-----	169
Db	526 ACAAATATTATAATACCAACCCCTTTACCAAGGAATTTTGGAAACCATTTTCACCTGCATCAT	585

170 GlnPheProThrIleAsnProAspGlnSerSerCysCysThrAsnAspAsnAsnIle 189

Db 586 CAGTCCCTACATCTCT---GATCAATCAGTTGTTCT----- 621

QY 190 AsnTyrTrpSerMetGluAspSerTrpSerMetGluLeuLeuAsnGlyAsp 206

Db 622 /ACTATGACCATGAAATCTTGTGACTTCA-CTACTAATGANGAT 671

RESULT 12

BM527508

LOCUS

544 bp mRNA linear EST 19-FEB-2002
 ba162ef08.y1 Gm-cl061 Glycine max cDNA clone SOYBEAN CLONE ID:
 Gm-cl061-3735 5' similar to TR:Q39028 Q39028 ATMYB2. ;, mRNA

DEFINITION

sequence.

ACCESSION

BM527508

VERSION

BM527508.1

KEYWORDS

GI:18733261

SOURCE

soybean.

ORGANISM

Glycine max

REFERENCE

1 (bases 1 to 544)

AUTHORS

Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Coryell,V., Khanna

TITLE

Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Coryell,V., Khanna

JOURNAL

Washington University School of Medicine

COMMENT

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

FEATURES

source

FEATURES

1. 544

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/lab_host="DH10B"

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/note="Vector: Bluescript II SK+; Site 1: EcoRI; Site 2:

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BASE COUNT 172 a 129 c 122 g 121 t

FEATURES

ORIGIN

FEATURES

Alignment Scores:

FEATURES

Pred. No.: 2,04e-81

FEATURES

Score: 779.50

FEATURES

Percent Similarity: 88.70%

FEATURES

Best Local Similarity: 84.75%

FEATURES

Query Match: 68.50%

FEATURES

DB: 13

FEATURES

Gaps: 3

FEATURES

US-10-021-811-36 (1-206) x BM527508 (1-544)

FEATURES

QY 1 MetAspIySylGlnGlnCysIySThrSerGlaAspProGluValArgIySgIyProTyr 20

FEATURES

Seq primer: -40RP from Gibco

FEATURES

High quality sequence stop: 422.

FEATURES

Location/Qualifiers

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